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                                                                                                                                                                                                                                                                                                                          481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 540
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                                                                                                                                                                                                                                                         361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
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                                                                                                                                                                                                                        181 CCAGTITCATACTCATGAGGGGIACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
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                                                                                                                                                                           0; Gaps
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Best Local Similarity 99.5%; Pred. No. 7.1e-196;
Matches 854; Conservative 0; Mismatches 4; Indels 0;
                                                                                 1. .4402/organism='Unidentified'.
                                                                           Location/Qualifiers
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| 984 c 1010 g 1069 t
                                                 C12N15/09, A61K48/00, C12N15/00 Strandedness: Both;
                          08-MAY-1998 JP 1998142134
                                                                                                    Location/Qualifiers
Unidentified
JP 1999318467-A/3
24-NOV-1999
                                                                     Topology: Linear;
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TTTTGTANSVIARAPSAQBALKKELETTTWYLEGSIGNAMHSEENDNQIRLAA
TTTTGTANSVIARAPSAQBALKKELTTTWYLEGSIGNAMHSEENDNQIRLAA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoffman, E.P., Monaco, A.P., Feener, C.C. and Kunkel, L.M. Conservation of the Duchenne muscular dystrophy gene in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
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                                                             1875 CCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 1934
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40.3%; Score 822.6; DB 10; Length 3275;
Best Local Similarity 86.7%; Pred. No. 7.8e-189;
Matches 906; Conservative 0; Mismatches 139; Indels 0;
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/db_xref="G1:192972"
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Mouse adult heart, cDNA to mRNA.
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                                                                                                                                                                                                                                                                 1995 ATCAAGTCTCGAGAAAGT 2012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841 ATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAGAAAAGAAAAAGCAATCCAT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           722 AGATCGATGGGCAAATATCTGCAGATGGACTGAAGACCGCTGGATTGTTTTACAAGATAT 781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAGA 480
                                                                                                                                                                                                                                            161 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                                                                                       122 TAGCATGGAAAACAAAGAAATTACACAAAGTTCTAATGGATCTCCAGAATT 481
                                                                                                                                                                                         1 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                               . TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
| TGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCAAATGATGTTGAAGAAGTGAAAGA 241
| 11 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 111
                                                                                            CCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
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Shortened dystrophin. E3021.1 G1:13017028 E30221.1 pt:13017028 unidentified.

> DEFINITION ACCESSION VERSION KEYWORDS

LOCUS

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1695 AGANGATCTAGAAGACCTAAAACGO AACAN AACAN
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SinichlyT.
Shortened dystrophin
Shortened dystrophin
Patent: JP 199318467-A 4 24-NOV-1999;
Patent: JP 199318467-A 4
SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
ON Unidentified
PN JP 1999318467-A/4
PD 24-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.3%; Score 658.8; DB 6; Length 4075;
nilarity 99.0%; Pred. No. 4.6e-149; Indels 0;
Conservative 0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1455 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGQ
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers / unidentified'.
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/db_xref="taxon:32644"
/db_910 f= 936 g
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Strandedness: Both;
                                                                                                                                                                                                          08-MAY-1998 JP 1998142134
                                                                                                                                                                                                                                                                                                                                 Topology: Linear;
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Best Local Similarity
Matches 663; Conserv
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661 AGATCGATGG 670

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="SKLIGTGKLSEDEETEVQEQMNLLNSRWECLRVASWEKQSNLHR
VLMDLQNQKLKELNDWLTKTEEETERTRKWEEEPLGPDLEDLKRQVQOHKVLQEDLEOEGE
RYNSLTHMVVVUDESSGHATAALEEQLKVLGPRWANICRWTEDRWVLLQDTLEVQCV
LTEEQCLFSAWLSEKEDAVNKIHTTGFKDQNEMLSSLQKLAVLKADLKWGN
107 c 142 g 140 t
                                           15/5 GRANDON TO THE SAGAR STANDAR SECTION OF THE SAGAR SECTION OF THE SA
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Deletions of fetal and adult muscule cDNA in Duchenne and Becker EMBO J. 6 (11), 3277-3283 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                    HSDWDF1
Human fetal mRNA fragment of DMD gene (DMD= Duchenne muscular
                                                                                                      1815 TACTGAGTGGGAAAATTGAACCTGCACTCGGCTGACTGGCAGAGAAAAATAGATGAA.
                                                                                                                                                                                                          1755 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAÄĞT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 AGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAG 319
                                                                                                                                                                                                                                                        661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAAGAAACTGAAGTACAAGAGAGGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Data kindly reviewed (12.0CT.1988) by DAVIES K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.6%; Score 624.2; DB 9;
99.5%; Pred. No. 1.2e-140;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                              1875 CCTTGAAAGACTCCAGGAACTTCAAGAGG 1903
                     1575 GAAAGAGTTGAATGACTGGCTAACAAAAA.
                                                                                                                                                                                                                                                                                                                       721 CCTTCTCAAATGGCAACGTCTTACTGAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/protein_id="CAA29545.1"
/db_xref="G1:30840"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X06179.1 GI:30839
Duchenne muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dev_stage="fetus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="DMD"
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Homo sapiens
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Best Local ;
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                                                                                                                       PAT 18-JUN-2001
                                                                                                                                                                                                        1 (bases 1 to 4402)
Sinich, T. 1 to 4402)
Sinich, T. 2 1 to 4402)
Sinich, T. 1 1 199318467-A 2 24-NOV-1999;
SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
TO 1999318467-A/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TGAAGTAAACCTGGACCGTTATGAAACAGCTTTAGAAGAAGTATTATCGTGGCTTGTTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 TGCTGAGGACACATTGCAAGCACAGAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B1 CCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGCATGGAAAAACAAAGGAATTTAGATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 4402;
                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism='Unidentified'.
                                                                                                             DNA
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Strandedness: Both;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.1%; Score 654.6;
92.1%; Pred. No. 4.8e
tive 0; Mismatches
                                                                                                      4402 bp
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/organism="unidentified"
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1000 c 1019 g
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                                                                                                       Shortened dystrophin.
E30219
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JP 1999318467-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                      Topology: Linear;
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1815 CACCAGATGG 1824
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690; Conservative
                                                                                                                                                            unidentified.
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PD
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                                               ESULT 4
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PRI 28-MAR-1991
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1966)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross, G.S., Speer, A., Rosenthal, A., Forrest, S.M., Smith, T.J., Edwards, Y., Flint, T., Hill, D. and Davies, K.E. Deletions of fetal and adult muscle cDNA in Duchenne and Becker muscular dystrophy patients
EMBO J. 6 (11), 3277-3283 (1987)
                                                                                                                                                                                                                                                                                                                                                  122 AATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGG 181
                                                                                                                               CTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTT 499
                                                                                                                                                                241
                                                                                                                                                                                                                242 GAAGACCTAAAACGCCAAGTACAACTACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAA 301
                                                                                                                                                                                                                                                                 CAAGTCAGGGTCAATTCTCTCACTCACATGGTGGTGGTGGTAGTTGATGAATCTAGTGGAGAT 619
                                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                               CACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1966 bp mRNA linear PRI 28 אואשה adult muscle mRNA fragment of DMD gene (DMD= Duchenne muscular dystrophy).
AATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGG
                                                                                                                                                 GAAGACCTAAAAACGCCAAGTACAACAAAAAAAGGTGCTTCAAGAAGATCTAGAACAAGAA
                                                                                                                                                                                                                                                                                TGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGT
                                                                                  Data kindly reviewed (12.0CT.1988) by DAVIES K.E.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602 GCCGTTTTAAAAGCGGATCTAAAAAAAA 630
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X06178.1 G1:30836
Duchenne muscular dystrophy.
Homo sapiens.
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1. .1966
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/ LTAIRS LATIONARY CONTROLLED EQUOR VNS. LTHWAV VVDESSGDHATAAL
EEQLKVLGDRWAN ICRATEDRWYLLQDILIKWQRLTEEQCESAKLSEKEDAVNKIHT
TGEKDONEMISSLQKLAVLKADLEKKKQSMCKLYSIKQDLLSTLKNKSVTQKTEAVNKIHT
TGEKDONEMISSLQKLAVLKADLEKKKQSMCKLYSIKQDLLSTLKNKSVTQKTEAWLD
NFARCWDNINQCKRQITVDSEIRKRLDVDITELHSWITRSEAVLQSPEFAIFRKEONFSDLK
EKVAALEREK REKFRKTQDASRSQQALVEQWNVEGVADSIKQASEDLNSRWIEFCQL
LSERLNWLEYQNNIIAFYNQLQCLEQMTTABNWLKIOPTPSEEPTAIFRKEONFSDLK
LSERLNWLESQLQNSTREKRQGSPWFLDADFVAFTNHFKQVFSDVQAREKELQT
IFOTLEPMRYQETMSAIRTWYQGSETKLSIPQLSVTDYEIMBQRLGELQARGREGQT
OGGLYYLZTTVKERGRKAPSEISRRYQSETBETBGRWKKLSSQLVBHCQKLEDQMNKL
RKIONHIOTILKKWMAEVDVFKEEWPALGDSETLKKQLKQCRLLVSDIQTIQPSLNSV
NEGGQKIKKNEAPERGSEISTRKQDFN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGATCTAGAAAAGAAAAGCAATCCATGGGCAAACTGTATTCACTCAAACAAGATCTTC 932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 AGTGCCTTTTTAGTGCATGGCTTTCAGAAAAAGAAGATGCAGTGAACAAGATTCACACAA 308
                                                                                                                                                                                                                                                                                                                                                                                           513 GCCAAGTACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCA 572
                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             9 GCCAAGTACAACAATAAGGTGCTTCAAGAAGATCTAGAAACAAGAACAAGAACTCAGGGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTGCCTTTTTAGTGCATGGCTTTCAGAAAAAGAAGATGCAGTGAACAAGATTCACACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 ATTCTCTCACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633 CTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCACAGA 1043
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                                                                                                                                                                                                                                                                                                                          25.9%; Score 527.8; DB 9; 99.6%; Pred. No. 2.9e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                             /db_xref="SWISS-PROT:P11532"
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
              /protein_id="CAA29544.1"
/db_xref="GI:30837"
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                                                                                                                                                                                                                                                                       443 g
/codon_start=2
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E30218
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Patent: JP 1999318467-A 1 24-NOV-1999;
SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1898)
Strausberg, R.
Direct Submission
Submitted (19-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                            61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
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                                                                                                                                                                                                                                                                                                                                      DB 6;
                                                                                                                                                                            Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Score 349.2; DB 6
Pred. No. 6.7e-74;
0; Mismatches 33
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                                                                                                                           C12N15/09,A61K48/00,C12N15/00
Strandedness: Both;

    .3747
    /organism="unidentified"

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                                                            24-NOV-1999
08-MAY-1998 JP 1998142134
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                               OMMENT
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 57 Row: p. Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
                                                                                                                                                                                                                     Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schelin, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AGTTCATTGATGGAGGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 GTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 CATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 TTATCGIGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAATGAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 CTGTCAGAGGAGGAGGAGTTTGAGATCCAGGAACAGATGACTTGCTGAATGCAAGGTGG 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409; Indels
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.9%; Score 344.6; DB 1 59.1%; Pred. No. 8.8e-73;
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/map="C57BL/6J"
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                             Contact: MGC help desk
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                                                                                                                                                                                                  info@bcgsc.bc.ca
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Danio rerio dystrophin (dmd) mRNA, partial cds, alternatively
524 CAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTCACT 583
              584 CACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTGTTTGGAAGAA 643
                                                          567 CACATGGTGATGTGGATGAAAACAGTGGGGAGAGTGCCACAGGTCTTCTGGAAGAT 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 CAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGG 703
                                                                                                      627 CAGTTACAGAAACTGGGTGAGGCTGGACAGCTGTATGCCGCTGGACTGAAGAACGTTGG 686
                                                                                                                                704 GTICTITIACAAGACAICCTICTCAAAIGGCAACGICTIACIGAAGAACAGIGCCTITII 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bolanos-Jimenez, F., Bordais, A., Behra, M., Strahle, U., Sahel, J. and
                                                                                                                                               687 AACAGGTIGCAAGAAATCAGTATICTGIGGCAGGAATTATTGGAAGAGCAGTGTCTGTIG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Direct Submission
Submitted (22-JAN-2001) Laboratoire de Physiopathologie Retinienne,
EMI 99-18 INSERM-Universite Louis Pasteur, 1, Place de l'Hopital,
Strasbourg 67091, France
Location/Qualifiers
                                                                                                                                                                            764 AGTGCATGGCTTTCAGAAAAAAAAGAAGGCGGGGGGAACAAGATTCACACAACTGGCTTTAAA 823
                                                                                                                                                                                       747 GAGGCTTGGCTCACCGAAAAGGAAGGCTTTGAATAAAGTTCAAACCAGCAACTTTAAA 806
                                                                                                                                                                                                                                   944 AAGAATAAGTCAGACCCAGAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGTTGG 1003
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
1 (Dases 1 to 3521)
                                                                                                                                                                                                                     824 GATCAAAATGTTATCAAGTCTTCAAAACTGGCCGTTTTAAAAGCGGATCTAGAA 883
                                                                                                                                                                                                                                                                884 aagaaaagcaatccatggggaaactgtattcactgaaacaagatcttctttcaacactg 943
                                                                                                                                                                                                                                                                                    867 Argadadgeacaeteridateaaeteaaeteaceaarteaceadaigiegeceaatraere 926
                                                                                                                                                                                                                                                                                                                                1004 GATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCACAG 1042
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Bolanos-Jimenez,F., Rendon,A. and Strahle,U.
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/db_xref="taxon:7955"
/chromosome="l"
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SSPSTAASPRSDTSLASLRVAASOTTETMGDDELSSPTGDASTGLEDVIEQIEDVIEGINNSFPHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1056 IGCAACAGTTCCCCCTGGACCTGGAAAGTTTCTTGCCTGGCTTACAGAAGCTGAAACAA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1116 CTGCCAATGTCCTACAGGATGCTACCCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAG 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1176 TAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATG 1235
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                                                                                                                                 /protein_id="AAK38376.1"
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/gene="dmd"
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On Sep 8, 1993 this sequence version replaced gi:213232.
Draft entry and computer readable sequence for [Unpublished (1990)]
Kindly submitted
by S.J. Burden, 06-AUG-1990.
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Ravin, A.J., Dyer, S.M., Yeadon, J.E. and Burden, S.J.
Multiple dystrophin isoforms are associated with the postsynaptic multiple dystrophin isoforms are associated with the postsynaptic membrane of Torpedo electric ordan membrane of Torpedo electric ordan J. Physiol. (Paris) 85 (3), 131-133 (1991)
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Torpedo californica dystrophin mRNA, 3' end.
M37645
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                                                                                                                                                          1776 AGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGC 1835
                                                                                                                                                                             1716 TCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATG 1775
                                                                                                                               1656 TGCCTCCTGAGGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGG 1715
1 (bases 1 to 2654) Year, S.M. and Burden, S.J. Yeadon, J.E., Lin, H., Dyer, S.M. and Burden, S.J. Dystrophin is a component of the subsynaptic membrane Dystrophin is a component (1991) J. Cell Biol. 115 (4), 1069-1076 (1991)
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Torpedo californica
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RESULT 11 HUMDYSTR15

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64.38;
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linear ROD 23-AUG-1995
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                                Direct Submission
Submitted (15-DEC-1994) D.J. Blake, Institute of Molecular
Medicine, Molecular Genetics, John Radcliffe Hospital, Oxford,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
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M.musculus mRNA for G-utrophin.
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Blake, D.J.
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           linear PRI 21-AUG-1995
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Roberts, R.G., Coffey, A.J., Bobrow, M. and Bentley, D.R. Genomics 16 (2), 536-538 (1993)
                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GDB:G00-119-850"
/translation="RFREEKTREPVIMSTLETVRIFLIEOPLEGLEKLYOEPRELPP
EBRAQNYTRILKRQAEEVNTEWEKLALHSADWORKIDETLERLOELOEDGEGLEKLYOEPRELPP
                                                                                                                                                                                                                         /map="Xp21.3-p21.1"

Join(L05636.1:1. 431,L05637.1:1. 384,L05638.1:1.

L05639.1:1. 434,L05650.1:1. 238,L05640.1:1. 275,

L05644.1:1. 339,L05642.1:1. 266,L05643.1:1. 275,

L05647.1:1. 360,L05645.1:1. 404,L05646.1:1. 447,

/qene="DMD" 360,L05648.1:1. 360,1. 500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1651 AGAGCTGCCTCCTGAGGAGAGGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGA 1710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 500;
HOMO Sapiens dystrophin (DMD) gene, exon 59.
                                                                                                                                                                                                                                                                                                                                                                                                                       QAEVIKGSWQPVGDLLIDSLQDHLEKVK"
order(L05648.1:255. >360,<1. 211)
                                                                                                                                                                                                                                                                                                        join(L05648.1:134. .254,212. .480)
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                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA74508.1"
/db_xref="G1:950346"
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                                                                                                                                                                                                                                                                                                                                                        /product="dystrophin"
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/note="G00-119-850"
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/note="G00-119-850"
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                       L05649.1 GI:181899
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                                                          Homo sapiens DNA.
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                                    dystrophin.
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3499 bp mRNA linear PRI 15-JUN-1996
Human dystrophin-related protein 2 (DRP2) mRNA, complete cds.
U43519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1900 AGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGT 1959
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1720 TACTGAGTGGGAAAAATTGAACCTGCTCCGCTGACTGGCAGAGAAAATAGATGAGAC 1779
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                                                                                                                                                                                                                                                                                                                                                 1609 GCAGCCTTT-----GGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCC 1659
                                                                                                                                                                                                                                                                                                                                                                                                       1549 GAMARCTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGA 1608
                                                                                                                                                                                                                                                                                                                                                                     749 TCAGCCAATAGAGGCCCCCGAAGAACCAAGAAGAAACCCACAATCAAAGAAGAAGTTGAC 808
                                                                                                                                                                                                                                                            1489 AGGGGACTITCCAGCAGTTCAGAAGCAGATGTACATAGGGCCTICAAGAGGAATT 1548
                                                                                                                                                                                                                                                                                                                          689 AAAGGAGAAAAGAGTATTCTGTGCTGAACGCCGTAGATCAAGCTCGAGTTTTTCTGGCTGA 748
                                                                                                                                                                                                                 629 AGGGANGTCCCTGCCTTACAGCTCCAATATGACCACTGCAAGGTGCTGAGACGTGAGCT 688
                                                                                                                                                                       1369 CATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTGCA 1428
                                                                                                                                                                                                                              569 AGAGCTGATCAATAGGCTCAATATGAAAGATGAGCAGTTGG 628
                                                                                                                            1309 ACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAA 1368
                                                                                                                                                                                   1249 GGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTT 1308
                                                                                                                                                  449 TCAGCATCGACTGATGACATGAACCAAAGATGGATTGAAGGCAAAATCTGCTAG 508
                                       389 CGATGGAAACCGGCAGAAGATGGTGAAAGCTCTGGGGAATTCTGAGGAAGCAACAATGCT 448
                                                           329 GAAGCICTGCAAGACATCCAGCAGAATTGATGCCCACAATGACATATTAAAAGCAT 388
                      9; Gaps
itch 13.1%; Score 267.6; DB 10; Length 3161; al Similarity 57.9%; Pred. No. 4.3e-54; Indels 9; 499; Conservative 0; Mismatches 354; Indels 9;
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/ AD_XTGET="G1:1333/82"

/ AD_XTGET="G1:1333/82"

/ APPODGAGVPCLSLKLLNGSVGASGPLEPPAMNLCWNEIKKKSHNLRRELEAFSDHSG

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KLQLPLQDEILDWLGSCORDELSAQLPELQGPVALVQGEKERWCATVASELWEKLTARCVD

CHRHIERTLSGHFFEELEEPHSESKOTTSOAGGVARTWRWCLGASVDERLKQLVD

CHRHIERTLSGHFFEELEEPHSESKOTTSOAGGVARTWRWCLGASVDERLKQLVD

CHRHIERTLSGHFFEELEEPHSESKOTTSOAGGVARTWRWCLGASVDERLKQLVD

CHRNIKFEELTGGAMELSTGWARTSPROKENTENTGOAGSVERWTELTGTLAD

CHRNIKFEELTGGAMELSTGWARTSPROKENTELTFALEIPWHDLOASEHWNDVEVLHGUTA

ANDREGGSCHGWARTSPROKALRLDLYTTTALEIPWHDLOASEHWNDVEVLHGUTA

ANDREGGSCHGWARTSPROKALRLDLYTTALEIPWHDLOASEHWNDVEVLHGUTA

ANDREGGSCHGWARTSPROKALRDLYTTALEIPWHDLOASEHWNDVEVLHGUTA

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KPVLESQTANGGSCCDQRHLGVLLHEATQVPROKGSTGROKTATLKNKFRSKHYFSK

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QFNVDICGTGTTGTGRAKGKNKHYPINETATASETTLRGHEBRENGLEBHESKRLETRRQTLEDG

ENDWSTGREDDOVLLRHSSFTTDREPREGGOARCSVTESKGELOKILAHLEDENRILDG

ENDRELDEDOVLLRHSSFTTDREPREGGGSGSGSGSHPREKGGTTPDTEAAD

BYGGSCQCQRURCHARSPTTSSGGSGSGSGSASSLASSSGSSGSHPREKGGTTPDTEAAD

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1327 CATGAACTTCAAGTGGAGTGAACTTCGGAAAAGTCTCTCAACATTAGGTCCCATTTGGA 1386
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Extraores: Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Extraores: Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 263 to 318)7.C., Kendall,E., Vetrie,D.L., Dixon,A.K., Shaw-Smith,C., Bone,Q. and Bobrow,M.
Shaw-Smith,C., Bone,Q. and Bobrow,M.
Caracterization of ppr2, a novel human dystrophin homologue Nat. Genet. 13 (2), 223-226 (1996)
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                                                                                                                                                                                                                     Coberts, R.G. 1 to 3499)

Roberts, R.G. 2 (bases 1 to 3499)

Direct Submission

Submitted (16-DEC-1995) Roland G. Roberts, Medical Genetics, Direct Submitted (16-DEC-1995) Roland Floor, Lab Block, Addenbrooke's Addenbrooke's Hospital, 3rd Floor, Cambs Cb2 20q, UK Hospital, Hills Road, Cambridge, Cambs Cb2 20q, UK Hospital, Hills Road, Cambridge, Cambs Cb2 20q, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"dystrophin-related protein 2"/protein_id="AAC50538.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="membrane cytoskeleton"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
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Roberts, R.G. and Sheng, M.
Direct Submission

Submitted (18-OCT-1999) Division of Medical and Molecular Genetics,
GKT Medical School, 8th Floor, Guy's Hospital, Guy's Tower, London
1507 TCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGAATTGAAAACTAAAGAACTGT 1566
                                                         1567 AATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGGAGCAGCCTTTGGAAGGACT 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                 1627 AGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGTCAC 1686
                                                                                                                                                                            1687 TCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCA 1746
                                                                                                                                                                                                                                     1747 CTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGA 1806
                                                                                                                                                                                                                                                                                              1807 GGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCA 1866
                       1867 GCCCGTGGGGGATCTCCTCATTGACTCTCCCAAGATCACCTGGAGAAAGTCAAGGCACT 1926
                                                                               792 CATCHATTCHGTGCHGAGTCAGCCTTCCTGTCCCAGCACCATTGAGGAGTT 851
                                                                                                                                         852 AGAGGAGCTCATTCTGAGAGCAAAGATACCTCCCGGAAACAGGGATCCAGAATCTCAG 911
                                                                                                                                                                                                                                                                                                                                                                                                                 1927 TCGAGGAGAAATTGGGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCA 1986
                                                                                                                                                                                             912 CCGCTTTGTATGGAAGCAGGCGACGGTGGCCAGTGAACTGTGGGAGAAGTTGACAGCCCG 971
                                                                                                                                                                                                                                                                                                                                                                         /gene="Drp2"
/note="splice acceptor AG dinucleotide used by A-form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus dystrophin-related protein 2 B-form splice AF195788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1987 GCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGA 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts, R.G. and Sheng, M. Association of dystrophin-related protein 2 (DRP2) with Postsynaptic densities in rat brain Mol. Cell. Neurosci. 16 (5), 674-685 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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LQGELRRLKWQHEEAVEAPTLAEGSAEATPDRRNEELLAEARILRQHKSRLETRMQIL
EDHNKQLESQLQRLRELLLQPPTESDGNGSAGSSLASSPRQSEGSHPREKGQTTPDTE
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/gene="Drp2"
/note="DRP2; membrane-associated cytoskeletal protein;
contains two spectrin repeats; WW domain; Z2 domain"
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                                                            /codon_start=1 //product="dystrophin_related protein 2 B-form splice
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/db_xref="GI:11066167"
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Matches 399; Conservative
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/translation-wADPLYMGGCPYTLPRCHEWHAADRFHHSSSLRNTCPOPOVRAAV
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KEKLQYLESQYANGGSKCORRLGALLHEAIQVPROLGEVAARGGSNVEPSYRSCFRF
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EDHNKOLESOLORLRELLLOPPTESDGNGSAGSSLASSPROSEGSHPREKGOTTPDTE
AADDVGSKSQDVSHSLEDIMEKLRHAFPSVRSSDVTANTLLAS"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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1927 TCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCA 1986
                             3140 bp mRNA linear ROD 02-Mi
Rattus norvegicus dystrophin-related protein 2 A-form splice
Ariant (Drp2) mRNA, complete cds.
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Roberts, R.G. and Sheng, M.
Association of dystrophin-related protein 2 (DRP2) with
Association of dystrophin ret brain
postsynaptic densities in rat brain
Mol. Cell. Neurosci. 16 (5), 674-685 (2000)
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267. .3140
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Best Local Similarity

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1100 CAAAGAAGAATTCTCTCTGTGAAAGACGGGGTGAAGTTAGTGAATGACTTGGCCCACCA 1159
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                            1327 CATGAACTTCAAGTGGACTGGAACTTCGGAAAAGTCTCTCAACATTAGGTCCCATTTGGA 1386
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                                                                                                                                    560 GGCCTTCTCAGACCACAGTGGAAAACTTCAGCTCCCACTTCAAGAGATTATTGACTGGCT 619
                                                              500 cargaarcrergranggaargaaaraaaaagaagrercacaaccrecceraga 559
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0; Mismatches 315; Indels
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Job time : 3532.87 secs
           Matches 399; Conservative
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(without alignments)
16150.348 Million cell updates/sec
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                                                                                                                                                                                                                            1 tccttcacagcatttggaag.....acctcagcactctggaagac 2041
                                                                                                               April 25, 2003, 07:25:57; Search time 284.596 Seconds
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| SIDS2/gcddata/geneseqy.geneseqn.embl/NA1983.DAT:*
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         2185239 seqs, 1125999159 residues
                                                                                                                                                                                       US-09-845-416-2_COPY_960_3000
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                                                                    OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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AAD37256
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1037.8 50.8 1991 24 AAD37231 Human dystrophin 999 48.9 2169 24 AAD37232 Human dystrophin 999 48.9 3531 24 AAD37238 Human dystrophin	851.6 41.7 4498 24 AAD37258 Aden 811.4 39.8 3275 10 AAD97129 Part 727 35.6 3510 24 AAD37240	727 35.6 4476 24 AAD37259 Adeno-associated	658.8 32.3 4075 21 AAZ48569 A.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C	052 31.9 1821 24 AAD37241 Human 390 19.1 1340 24 AAD37239 Human	347 19.0 387 24 ABK81990 Human 349.2 17.1 3747 21 AAZ48566 A FOO	348 17.1 348 24 ABK81989 Human 333 16.3 333 24 ABK81967	327 16.0 327 24 ABK81966 Human 322.4 15.8 333 24 ABK81968 Human	265 13.0 1434 24 AAD37243 Human	198.2 9.7 1500 22 AAF84672 Nucle	190.2 9.3 256 22 ABA69736 Human 190.2 9.3 256 22 ABA69736	190.2 9.3 256 22 AAK17925 Himan	190.2 9.3 256 22 AAK43799 Human	190.2 9.3 256 22 AAI24574 Probe	190.2 9.3 256 24 ABS18027 Human	177 8.7 466 23 ABS08442 Human	177 8.7 466 22 ABA27626 Human	177 8.7 466 22 AAK06756 Human	177 8.7 466 22 AAR32467 Human bone marrow	177 8.7 466 22 AAI38301 Probe	ALIGNMENTS	T 1	230 AAD37230 standard, DNA, 4182 BP.	D37230;	$21 ext{-AUG-}2002$ (first entry)	Human dystrophin minigene delta4173.	Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Gecker muscular dystrophy; ds.	Homo sapiens.	VO200183695-A2.)8-NOV-2001.	77-APR-2001; 2001WO-US13677.	8-APR-2000; 2000US-200777P.	XIAO/) XIAO X.	.iao X;	PI; 2002-049342/06.	
0	83	9	65		34		32		119	4 11	96	7 -	19(19(, , ,	-1-	, ,	_		RESULT 1	.0 .D3723	D3723	-AUG-2	тап		S OII	2001	- NOV -	-APR-	-APR-2	[AO/)	õ	; 200	XX

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain,

a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domains and cysteine-rich domains of dystrophin or utrophin genes. The dominis and cysteine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to a expression control element, in a recombinant adeno-associated virus or retrovirus is control element, in a mammalian destrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta4173 containing nucleotides 1:1992 (N-terminus, hinge H1 and rods R1, R2 and R3), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids). repeats, H1 and H4 domains and a cysteine rich domain of Example 1; Page 43-44; 71pp; English. rod repeats, Hl an dystrophin gene ·

Sequence 4182 BP; 1309 A; 927 C; 970 G; 976 T; 0 other;

0; Gaps 100.0%; Score 2041; DB 24; Length 4182; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels 0; Matches 2041; Conservative Local Similarity Query Match

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121 TGCTGAGGACACATTGCAAGCACAAGGAGAGTTTCTAATGATGTGGGAAGTGGGTGAAAGA 180

241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300

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AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 1319 360 **AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC** 301

TAGCATGGAAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 1379 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 1320 361

420

GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCCAAGTACAACAACATAAGGTGCTTCA 540 421

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601 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG

840 781 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTT qq

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1860 GGGCAAACTGTATTCACTCAAACAAGATCTTTCAACACTGAAGAATAAGTCAGTGAC 1919 GGGCAAACTGTATTCACTCAAACAAGATCTTCTTCAACACTGAAGAATAAGTCAGTGAC 960 901 g ò δy

1980 ACTIGAAAAGAGIACAGCACAGACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGA 1021 ACTIGAAAAGAGIACAGCACAGACTCATAGAITACIGCAACAGITCCCCCIGGACCTGGA

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1081 AAAGTTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTAC 1140 2040 AAAGTTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTAC 2099 1141 CCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCA 1200 qq

1201 AGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAG 1260 q

1261 CCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTT qq δy

1321 GGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCA 1380 qq Óλ

qq

δy

1441 GIGGCTACAGCIGAAAGAIGAIGAATIAAGCCGGCAGGCACCTATIGGAGGCGACITICC 1500 g δ

accigiaatcaigagiactcitgagactgtacgaatatttctgacagagcgtttgga 1620 1501 AGCAGTICAGAAGCAGAACGAIGTACAIAGGGCCTICAAGAGGGAATIGAAAACTAAAGA QQ δ

1561

δλ

AGGACTAGAGAAACTCTACCAGGAGCCCAGAGGCTGCCTCCTGAGGAGAGAGCCCAGAA 1680 1621 QΥ g

1681 TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAA 1740 2640 TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGGAAAATTGAA 2699 qq οy

Οy q

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1801 TCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGAAGCTGAGGTGATCAAGGGATC 1860 QY 4;

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1861 CTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAA 1920
                                2820 CTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCCCCAAGATCACCTCGAGAAAGTCAA 2879
                                                      1921 GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGC 1980
                                                               2880 GGCACTTCGAGGAGAATTGCGCCTCTGAAGAGAACGTGAGCCACGTCACGTCATGACCTTGC 2939
                                                                                     1981 TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGA 2040
                                                                                              2940 TGGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTTGGAAGA 2999
                                                                                                                                                                                                                                           Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                       New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain,
                                                                                                                                                                                                                           Human dystrophin minigene delta3990.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 46-47; 71pp; English.
                                                                                                                                                                          AAD37234 standard; DNA; 3999 BP.
                                                                                                                                                                                                                                                                                                                                         28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                         27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                           21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-049342/06.
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The present invention relates to an isolated nucleotide sequence encoding of a dystrophin minigene. The minigene comprises N-terminal or modified domains and cystaine-rich domains, utrophin or a spectrin gene, HI and H4 commissing dystrophin minigene operably linked to an expression corrol element, in a recombinant adeno-associated virus (AAV)

CC control element, in a recombinant adeno-associated virus or retrovirus is control element, in a recombinant adeno-associated virus or retrovirus is dystrophy (BMD) in a mammalian subject. The present sequence is human cystrophy (BMD) in a mammalian subject. The present sequence is human and cods RI and R2), 8059-10227 (rods R22, R33 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

Sequence 3999 BP; 1223 A; 907 C; 933 G; 936 T; 0 other;

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1921 GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGC 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2697 GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAAGGTGAGCGACGTCAATGACCTTGC 2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1861 CIGGCAGCCGTGGGCGATCTCCTCTCTCTCCAAGATCACCTCGAGAAGTCAA 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1741 CCTGCACTCCGCTGACTGGCAGAAAAATAGATGAGACCTTGAAAGACTCCAGGAACT 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1801 TCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATC 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2457 TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGGTCAATACTGAGTGGGAAAATTGAA 2516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1681 IGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAA 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                    1621 AGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAA 1680
                                                                                                                                                                                                                                                                                                                                                                               1561 ACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGA 1620
                                                                                                                                                                                                                                                                                                                                                                                           2337 ACCIGTAATCATGAGTACTCTTGAGACTGTACGAATATTCTGACAGAGCAGCCTTTGGA 2396
                                                                                                                                                                                                                                                                                                                                      1501 AGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGA 1560
                                                                                                                                                                                                                                                                                                                                                2157 TITGGAAGCAGTTCTGACCAGGAAGCTCTGCACCTTTCTCTCTGCAGGAACTTCTGGT 2216
                                                                                                                                                                                                                    2097 GGATAACATCAAGTGGAGTGAACTTCGGAAAAGTCTCTCAACATTAGGTCCCA 2156
                                                                                                                                                                                                                                                  1381 ITTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGT 1440
                                                                                                                                                                                                        1321 GGATAACATGAACTTCAAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCA 1380
                                                                                                                                                                          2037 CCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTT 2096
                                                                                                                                                               1261 CCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGAGGTTT 1320
                                                                                                                     1201 AGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAG 1260
                                                                                                                                 1977 AGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAG 2036
                                                                                      1917 CCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCA 1976
                                                                          1141 CCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCA 1200
                                1081 AAAGTITCTTGCCTGGCTTACAQAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTAC 1140
                                            1857 AAAGTTECTEGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTAC 1916
2041 C 2041
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RESULT 3

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 and the main and the comprise of dystrophin or utrophin genes. The comprising dystrophin minigene operably. Linked to an expression control invention also relates to a recombinant adeas of the according to a recombinant control comprising dystrophin minigene in operably linked with an expression control element. The dystrophin minigene in operably linkage with an expression control element in a recombinant adosonassociated virus or retrovirus is useful for treating buchenne muscular dystrophy (BWD) in a mammalian subject. The present sequence is AAV exprophy (BWD) in a mammalian subject. The present sequence is AAV evector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1897 CCAGTTCATACTCATGAGGGTACATGATGATTTCACAGCCCATCAGGCCCGGGTTGG 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1837 IGCTGAGGACACTGCAAGGAGAGAGTTTCTAATGATGTGGAAGTGGTGAAAGA 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1717 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGAGAG 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TGCTGAGGACACATTGCAAGGACACATTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCCTTCACAGCATTTGGAAGGTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72; Indels 183; Gaps
                                                                                                                                                                                   spectrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; dystrophin minigene; muscular; gene therapy; utrophin; spect adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4966 BP; 1403 A; 1216 C; 1232 G; 1115 T; 0 other;
                                                                                                                                        Adeno-associated virus vector plasmid, AAV-MCK-delta3990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 59-60; 71pp; English.
AAD37256 standard; DNA; 4966 BP.
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                                                                                                                  21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                              Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dystrophin gene -
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2854 GGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCA 2913
                            1381 TITGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTGTGGAAGCTTCTGGT 1440
                                          2914 TTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGT 2973
                                                                                 1441 GTGGCTACAGCTGAAAGATGAATTAAAGCCGGCAGGCACCTAATTGGAGGCGACTTTCC 1500
                                                                                               3034 AGCAGTICAGAAGCAGCAAGGATGTACATAGGGCCTTCAAGAGGGAATTGAAAGTTAAAGA 3093
                                                                                                                                       1501 AGCAGTTCAGAAGCAGGAGGTGTACATAGGGCCTTCAAGAGGGGAATTGAAAACTAAAGA 1560
                                                                                                                                                                                             1561 ACCIGIAATCATGAGACTCTTGAGACTGTACGAATATTTCTGACAGGGGGCCTTTGGA 1620
                                                                                                                                                                                                           3094 ACCIGTAATCAIGAGTACTCTIGAGACTGTACGAATATTTCTGACAGAGCAGCCTTIGGA 3153
                                                                                                                                                                                                                                                  1621 AGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAA 1680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD37262 standard; DNA; 4990 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Homo sapiens.
Chimeric - Cytomegalovirus.
Chimeric - Unidentified.
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27-APR-2001; 2001WO-US13677.

中义员

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 of N-terminal domains, rod repeats, utrophin or atrophin gene, The domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is control element, in a recombinant adeno-associated virus or retrovirus dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a vector plasmid construct containing human dystrophin minigenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATGGTGGCTTCTTC 120
                                                                                                                                                                                               New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCCTTCACAGGATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 74.5%; Score 1519.8; DB 24; Length 4990; Best Local Similarity 87.5%; Pred. No. 0; Marches 72; Indels 183; Comatches 1786; Conservative 0; Mismatches 72; Indels 183; Comatches 183; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4990 BP; 1439 A; 1185 C; 1208 G; 1158 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 67-68; 71pp; English.
28-APR-2000; 2000US-200777P.
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                                                                                                                                                                                                                                                                                                                                     dystrophin gene .
                                                                      (XIAO/) XIAO X.
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                                                                                                                                                                                               2509 GACTGTTACTCTGGTGACACA-----ACCTGTGGTTACTAAGGAAACTGCCATCT- 2558
                                                                                          2461 GCCTGAC-----CTAGCTCCTGGACTGACCACTATTGGAGCCTCTCCTACTCA 2508
                                                                                                                                                                                                                                                                  901 GGGCAAACTGTATTCACTCAAACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGAC 960
                                                                                                                                                                                                                      781 AAAAGAAGAAGAAGAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTT 840
721 CCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 780
                                                                               661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACGCTGGGGTTCTTTACAAGACAT 720
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                                                                                                                             g
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3238 TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAA 3297
                       1681 TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAA 1740
                                                                              3178 AGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCGAGAGGAGAGAGCCCAGAA 3237
                                                                  1741 CCTGCACTCCGCTGACTGGCAGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACT 1800
                                                                                                             1801 TCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATC 1860
                                                                                                                         3358 TCAAGAGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAAGGGATCAAGGGTT 3417
                                                                                                                                                         1861 CTGGCAGCCCGTGGGCGATCTCCTTGACTCTCCAAAATCACCTCGAGAAAGTCAA 1920
                                                                                                                                                                    3418 CTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAA 3477
                                                                                                                                                                                                     1921 GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAACGTGAGCCACGTCAATGACCTTGC 1980
                                                                                                                                                                                                                 3538 TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGGACTCTGGAAGA 3597
                                                                                                                                                                                                                                                1981 TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGA 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, HI and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human dystrophin minigene delta3849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 48-49; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                          AAD37237 standard; DNA; 3858 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200183695-A2.
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                                                                                                                                                                                                                                                                                              2041 C 2041
                                                                                                                                                                                                                                                                                                                    3598 C 3598
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                                                                                                                                                                                                                                                                                                                                                                                                  AAD37237;
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV)

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comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Backer muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3849 containing nucleotides 1-1668 (N-terminus, and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                     1020 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 1079
                                                                                                                                                                                                                                                                                                     61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
                                                                                                                                                                                                                                                                                        121 TGCTGAGGACACATTGCAAGGACACAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1260 AACTGAAGTACAAGAGCAGATGAAGTCCCTAAATTCAAGATGGGAATGCCTCAGGTAGC 1319
                                                                                                                                                                                                                                                                                                                                         181 CCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels 324; Gaps
                                                                                                                                                                                       1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AACTGAAGTACAAGAGGAGATGAATGTGCTAAATTCAAGATGGGAATGGCTCAGGGTAGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAAAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1620 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTGTTTTACAAGAC-- 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 TGATGAATCTAGTGGAGATCACGCAACTGCTGTTTGGAAGAACAACTTAAGGTATTGGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTACAAGACAT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 CCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             841 ATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAGAAAAGAAAAAGCAATCCAT 900
                                                                                                                                                Score 1383; DB 24; Length 3858;
Pred. No. 0;
                                                                                                            Sequence 3858 BP; 1189 A; 866 C; 905 G; 898 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1678 ------
                                                                                                                                                         84.1%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                              67.88;
                                                                                                                                                             Matches 1717; Conservative
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1861 CIGGCAGCCGIGGGCGAICICCICATIGACICICCCAAGAICACCICGAGAAGICAA 1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1741 CCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACT 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1681 TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGGGCTCAATACTGAGTGGGGAAAATTGAA 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1621 AGGACTAGAGAAACTOTACCAGGAGCCCAGAGAGCTGCCTGAGGAGAGAGAGCCCAGAA 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1501 AGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGA 1560
                                                                                                                                                                                                                                                                                                                                                                                                                1561 ACCIGIAAICAIGAGIACTCIIGAGACIGIACGAAIAITICIGACAGAGAGAGCIITIGGA 1620
                                                                                                                                                                                                                                                                                                                         1381 TTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTTGCAGGAACTTCTGGT 1440
                                                                                                                                                                                                                                                                                             CCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTT 1320
                                                                                                                                                                                                                                                      1321 GGATAACATGAACTTGAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCA 1380
                                                                                                                                                                                                     1201 AGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAACAG 1260
                                                                                                                                                                                                               1141 CCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGGTGATGAAACAATGGCA 1200
                                                                                                                                                                          1021 ACTIGAAAAGAGTACAGCACAGACTCATAGATTACTGGAACAGTTCCCCCTGGACCTGGA 1080
                                          961 CCAGAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAA 1020
     901 GGGCAAACTGTAFTCACTCAAACAAGATCTTTCAACACTGAAGAATAAGTCAGTGAC 960
1678 ------
                                      1678 -----
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 Gomains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) invention also relates to a recombinant adeno-associated virus (AAV) invention also relates to a recombinant adeno-associated virus or extression comprising dystrophin minigene in operable linkage with an expression element. The dystrophin minigene in operable linkage with an expression useful for treating buchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle vector plasmid construct containing human dystrophin minigenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, or cod repeats, HI and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCCTTCACAGGATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels 324; Gaps
creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 4825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 4825 BP; 1369 A; 1175 C; 1204 G; 1077 T; 0 other;
                                                                                                                                                                                                                                                                         Adeno-associated virus vector plasmid, AAV-MCK-delta3849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.8%; Score 1383; DB
84.1%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 61-62; 71pp; English.
                                                                                                                                                                                       AAD37257 standard; DNA; 4825 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 84.1
Matches 1717; Conservative
                                                                                                                                                                                                                                                        21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dystrophin gene <sup>-</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200183695-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                   2676 C 2676
                                                                                    2041 C 2041
                                                                                                                                                                                                                            AAD37257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xiao X;
                                                                                                                                                                      RESULT 6
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SAGATTTCTAATGATG	GATGGATTGATGATGTGGAAGTGGTGAAGA 189 GATGGATTGACAGCCCATCAGGGCCGGGTTGG 240 GATGGATTTGAAACCCATCAGGCCGGTTTG 240	ACAGGAAAATTATCAGAGGCCGGGTTGG 1	OY 301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGAAATTAAGAGGAATGAAGA 2016 Db 2017 AACTGAAGTACAAGAGCAAAGAAGAAAAAAAAAAAAAAA	361 TAGCATGGAAAAACAAAGCAATTTACATAGATTTAAATTCAGGGATGCCTCAGG	421 GAAGGGTTGAATGACTGAACAAAAGGGATCTCCAGAATCAGAAACAGAAACAGAAACAGAAACAGTTGAATGATGATGACTGCCTAACAAAAACAGAAAGAGAAAGAGTTGAATGATTATTTTTTATTTTTTTT	481 GCCTCTTGGACCTGATCTTGAAGACGCAAAATC 2197 GITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	541 AGAAGATCTAGAACAAGAAGACCTAAAAGACGCCAAGTACAACAACAACAAGAGGTGC	2257 AGAAGATCTAGAAGAAGAAGAAGAGAGGTCAGTTCTCTCATTCAGATGGTGGTAGTAGT 600	601 TGATGAATCTAGTGGAGATCACGCAACTGCTTGCAAGAAGAACAACTAAGGTTTGGGAAGAGAACAACTTAAGGTATTGGG 660 2317 TGATGAATCTAGGAGATCACGCAACTGCTGCTTTTTTTTT	STATTGG	721 CCTTCTCAAATGGCAACGTCTT	roligangaACAGTGCCTTTTTAGTGC	AAGATTCACACAACTGGCTTTAAAGATCAAAATCAAAATTCAAAATTTAAAGATTCAAAAATTAAAAAAATTAAAAAAAA		TCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAGAAAAAAAA	901 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 388 0000 388 0000 388 0000 388 0000 388 0000 388 0000 388 00000 380 0000 388 0000 380 0000 380 0000 380 0000 380 0000 380 00000 380 0000 380 0000 380 0000 380 0000 380 0000 380 0000 380 0000	35	AAGCATGGCTGGATAACTTTGCCCGGGTGTTTCCAATAAATTTTCCCCCGGTGTTTCCAATAAACTTTGCCCCGGTGTTTCCAATAATTTTCCAATAATTTTCCAATAATTTTCCAATAAT		CAGTTCCCCT	CTGGACCTGGA 247	2473 AAAGTTTCTTGCCTGGCTTACAGAAGCTGAAACAGCTGCCAATGTCCTACAGGATGTTCTTAC 2532	COLTANOGAMOGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCA 12 	459
J	J 1	O D	0 0	OY OP	QY Db	oy do	Qy	Op	QV Dp	Qy	٥y	Dp	0	QQ	oy D	0	2 a	δy	Dp	Qy Db	Οy	qo ^o	qq	

_	Oy 120	1 AGACCICCAAGGTGAAATTCAACTTCA
_	Db 259	
~	Oy 126	GATGTTATCACAACCTGGAT
1	Db 2653	32
J	0y 1321	GGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAACTCTCTTGTTACAAAGGCGTTT 271
Ц	Db 2713	GGATAACATGAACTTCAACGTGGAACTTCGGAAAAACTTTGGGAACAACAACAACAAAAAAAA
α	Qy 1381	TTTGGAAGCCAGTTCTGACCAGTGGAAGCGTTTTGCAACTTTTTTTT
Ω	Db 2773	TTTGGAAGCCAGTTCTGAAGCGTGTGGAAGCGTGTTGTGTTTTTGGAAGCCAGTTTTTGGAAGCCAGTTTTTTTT
δλ	y 1441	TGGCTACAGCTGAAAGATGATGAATTAAAGCCGCAAAAAAAA
qα	b 2833	50
Οy	1501	289
qq	2893	56
δλ	, 1561	295
QQ	2953	TGTAATCATGAGTACTCTTGAGACTGTACGAATATTTGTGACAACAACAAAAAAAA
Οŷ	1621	COTTABLE STATE OF STA
qq	3013	GAA 168
ΟY	1681	SCIENCAGEGGGGGCCCCAGAA 307
qq	3073	3TCACTCGGCTTCTACGAAAGCAGCCTGAGGGGGTCAATATTTAA 174
Οy	1741 (3AA 313
QO	3133 (3CACTCCGCTGACTGGCAGAAAAATAGATGAGACCCTTTGAAACACTCCAGGAAGT 180
Qγ	1801	GAGGGGCTCCAGGAACT 319
QQ	3193 1	86
Οy	1861 C	GAGGIGATCAAGGGATC 325
DP	3253 C	92
δŽ	1921 G	CGAGAAAGTCAA 331
Dβ	3313 G	TTGC 198
δλ	1981 T	AATGACCTTGC 337
QΩ	3373 T	TGGAAGA 204
δy	2041 C	
QQ	3433 C	3433
RESU AAD3	LT 7 7263 AAD3726	3 standard; DNA: 4848 pp
AC AC	AAD3726	3;
X	21-AUG-	2002 (first entry)
DE XX	Adeno-a	ssociated virus (AAV) vector plasmid, AAV-CMV-delta3840
ΚW	Human; (gene therapy; utronhing snorth;
		Ola (Idamo)

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cystelne-rich domains of dystrophin or utrophin genes. The domains and cystelne-rich domains of dystrophin or utrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control comprising dystrophin minigene in operable linked to an expression control control lement, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV dystrophy (BMD) in a mammalian subject. The present sequence is AAV coetor plasmid construct containing human dystrophin minigenes, a cytomegalovirus (CMV) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2040 AACTGAAGTACAAGAGGAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 2099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1980 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1800 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1860 TGCTGAGGACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CCAGITICAIACICAIGAGGGGTACAIGAIGGAITIGACAGCCCAICAGGGCCGGGIIGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                     New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G7.8%; Score 1383; DB 24; Length 4848; Similarity 84.1%; Pred. No. 0; O; Indels 324; Gaps 17; Conservative 0; Mismatches 0; Indels 324; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4848 BP; 1405 A; 1144 C; 1180 G; 1119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 68-70; 71pp; English.
                                    Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                      28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                    27-APR-2001; 2001WO-US13677
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                                                                                          Chimeric - Cytomegalovirus.
                                                                                                          Chimeric - Unidentified.
                                                                        Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dystrophin gene -
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                                                                                                                                               781 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTT 840
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                                                                                                                                                                                                                                         661 AGATGGATGGGCAAACATCTGTAGATGGACAGAAGACGGCTGGGTTCTTTACAAGACAT 720
                                       2160 GAAAGAGTIGAATGACTGGCTAACAAAAACAGAAGAACAACAACAAAAATGGAGGAAGA 2219
                                                                                                                                                                                      601 TGATGAATCTAGTGGAGATCACGCAACTGCTGTTTGGAAGAACAACTTAAGGTATTGGG 660
2100 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATGTCCAGAAATCAGAAACT 2159
                                                                                                                                 481 GCCTCTTGGACCTGATCTTGAAGACCTAAAAGGCCAAGTACAACAACATAAGGTGCTTCA 540
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1501 AGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGA 1560
              2916 AGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGA 2975
                                              1561 ACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGA 1620
                                                           2976 ACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGAGCGCCTTTGGA 3035
                                                                                           1681 TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGATCAATACTGAGTGGGAAAAATTGAA 1740
                                                                                                                                                     1741 CCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACT 1800
                                                                                                                                                                                                   3156 CCTGCACTCCGCTGACTGCCAGAGAAAATAGATGAGACCCTTGAAGACTCCAGGAACT 3215
                                                                                                                                                                                                                                                3216 TCAAGAGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGTCA 3275
                                                                                                                                                                                                                                   1801 TCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATC 1860
                                                                                                                                                                                                                                                                               1861 CTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAA 1920
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                                                                                                                                                                                                                                                                                                                              1921 GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCCACGTCAATGACCTTGC 1980
                                                                                                                                                                                                                                                                                                                                           3336 GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAGAGGAGCGTGAGCACGTCAACGTCAATGACCTTGC 3395
                                                                                                                                                                                                                                                                                                                                                                           1981 TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGA 2040
                                                                                                                                                                                                                                                                                                                                                                                       3396 TCGCCAGCTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCTGAGAAAA3455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adeno-associated virus vector plasmid, AAV-MCK-3447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD37260 standard; DNA; 4414 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Homo sapiens.
Chimeric - Unidentified.
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H and H4 domains and cysteine-rich domains of dystrophin or utrophin gene, H and H4 comprising dystrophin minigene operably linked to an expression control celement. The dystrophin minigene in operable linkage with an expression control useful for treating Duchenne Muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammanian subject. The present sequence is AAV creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                        ó
New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                      1717 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGAAGA 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1777 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTTTT 1836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                      1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2077 TAGCATGGAAAACAAAGCAATTTACATAGATTTTAATGGATCTCCAGAATGAGAACT 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TAATAITCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCGAGAATCAGAAACT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 TGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGG 660
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                                                                                                                                                                                                                                                                                                                                            DB 24; Length 4414;
                                                                                                                                                                                                                                                                                             Sequence 4414 BP; 1255 A; 1075 C; 1086 G; 998 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                  51.6%; Score 1054; DB 24;
96.8%; Pred. No. 3.2e-282;
tive 0; Mismatches 35;
                                                                       Example 1; Page 65-66; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                              Conservative
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin miniqene. The miniqene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin miniqene operably linked to an expression control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                2737 ACTIGAAAAGAGTACAGCACAGACCCTIGAAAGACICCAGGAACITCAAGAGGCCACGGA 2796
                                                                                                                                                                                                                                2677 CCAGAAAGACGGAAAGCATGGCTGGTGTTGGCATAATTTAGTCCAAAA 2736
                                                                                                                                                                                                                                                                       1021 ACTIGAAAAGAGTACAGCACAGACTCATAGATTACTGGAACAGTTCCCCCTGGACCTGGA 1080
                                                                                                                                                                           2617 GGGCAAACTGTATTCACTCAAACAAGATCTTCTTCAACACTGAAGAATAAGTCAGTGAC 2676
                                                                                                                                                                                                                 961 CCAGAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAA 1020
                                                                                                                      841 ATCAAGTCTTCAAAAAGTGGCCGTTTTAAAAGCGGATCTAGAAAAGAAAAAAGCAATCCAT 900
                                                                                                                                                              901 GGGCAAACTGTATTCACTCAAACAAGATCTTTCAACACTGAAGAATAAGTCAGTGAC 960
                                                    781 AAAAGAAGATGGAGTGAACAAGATTCACACAGGGTTTAAAGATCAAAATGAAATGTT 840
721 CCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 780
                                                                                                                                                                                                                                                                                                                                       1081 AAAGTTTCTTGCCTGGCTTACAGAAGCTGA 1110
                                                                                                                                                                                                                                                                                                                                                                2797 TGAGCTGGACCTCAAGCTGCGCCAAGCTGA 2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 53-54; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human dystrophin minigene delta3447.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD37242 standard; DNA; 3446 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTT 840
element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta347 containing nucleotides 1-1992 (N·terminus, hinge HI and rods RI, R2 and R3), 8749-10227 (rod R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1439 GCCTCTTGGACCTGATCTTGAGGCCTAAAGGCCCAAGTACAACATAAGGTGCTTCA 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTACAAGACAT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1260 AACTGAAGTACAAGAGCAGATGAATCCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                                                                                            361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                   301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                      1020 TGAAGTAAACTGGACCGTTATCAAACGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 1079
                                                                                                                                                                                                                                                                                                                                                 241 TAATATICTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                           181 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGCCGGGTTGG 240
                                                                                                                                                                                                                                                      121 TECTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                           61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
                                                                                                                                                               1 TCCTTCACAGCATTIGGAAGCTCCTGAAGACAAGTCATTIGGCAGTTCATTGAIGAGAG 60
                                                                                                                    51.1%; Score 1042; DB 24; Length 3446; 96.8%; Pred. No. 6e-279; Live 0; Mismatches 35; Indels 1;
                                                                                                Sequence 3446 BP; 1074 A; 766 C; 787 G; 819 T; 0 other;
                                                                                                                                           Best Local Similarity 96.8%;
Matches 1074; Conservative
                                                                                                                                        Query Match
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1859 GGGCAAACTGTATTCACTCAAAGATCTTCTTTCAACACGAGAATAAGTCAGGGAC 1918
                         961 CCAGAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAA 1020
                               1021 ACTTGAAAAGAGTACAGCAGACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGA 1080
                                                        901 GGGCAAACTGTATTCACTCAAACAAGATCTTTTCAACACTGAAGAATAAGTCAGTGAC 960
                                                                                                                                                         Human dystrophin N-terminus, hinge, and rod regions encoding DNA #1.
                                                                          1081 AAAGTTTCTTGCCTGGCTTACAGAAGCTGA 1110
                                                                                     2039 TGAGCTGGACCTCAAGCTGCGCCAAGCTGA 2068
                                                                                                                    AAD37231 standard; DNA; 1991 BP.
                                                                                                                                             21-AUG-2002 (first entry)
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
Becker muscular dystrophy; ds.

Homo sapiens.

WO200183695-A2.

08-NOV-2001.

27-APR-2001; 2001WO-US13677.

28-APR-2000; 2000US-200777P.

(XIAO/) XIAO X.

WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a

Example 1; Page 45; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N terminal or modified N terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 invention also relates to domains of dystrophin or utrophin genes. The Comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (DMD) in a mammalian subject. The present sequence is human dystrophin DNA fragment encoding N-terminus, hinge HI and rods RI, R2

Sequence 1991 BP; 680 A; 393 C; 442 G; 476 T; 0 other;

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Gaps
        50.8%; Score 1037.8; DB 24; Length 1991;
99.8%; Pred. No. 6.6e-278;
tive 0; Mismatches 2; Indels 0; C
                                              Conservative
Query Match
Best Local Similarity
Matches 1039; Conserv
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61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATGGTGGCTTCTTTC 120
                                                                                                                                   121 TGCTGAGGACACATTGCAAGCACAAGGAGAGTTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                  181 CCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                 241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                         301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                         361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                                              421 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAACAAGGAAAATGGAGGAAGA 480
                                                                                                                                                                                                                                                       481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                                                                                                                           601 TGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAAGTATTGGG 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             841 ATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAGAAAAGAAAAAGCAATCCAT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              901 GGGCAAACTGTATTCACTCAAACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGAC
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified a dystrophin minigene. The minigene comprises N-terminal or modified domains, rod repeats, utrophin or a spectrin gene, H and H4 N-terminal domains, rod repeats, utrophin or utrophin genes. The domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adency associated virus (AAV) invention also relates to a recombinant in noperable linkage with an expression control element. The dystrophin minigene in operable linkage with an expression useful for treating Duchenne muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin DNA fragment encoding rods R22, R23 and R24, hinge H4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1223 GCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1163 GACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACTCCAAGGTGAAATTGAA 1222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 GCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human dystrophin rod, hinge and CR domain regions encoding DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.9%; Score 999; DB 24; Length 21 ilarity 100.0%; Pred. No. 4.3e-267; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2169 BP; 623 A; 529 C; 524 G; 493 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 45-46; 71pp; English.
                           AAD37232 standard; DNA; 2169 BP.
                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-2000; 2000US-200777P.
                                                                                                             21-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR domain regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dystrophin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                             WO200183695-A2
                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                            AAD37232;
RESULT 11
                       AAD37232
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
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                                                                                                                                                                                                                                                                                                                                                                                            1823 GACCICAAGCIGCGCCAAGCIGAGGTGATCAAGGGATCCIGGGAAGCCGGTGGGGGATCTC 1882
                                                                                                                                                                                                                                                                                                      1763 AGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTG 1822
                                                                                                                                                                                                                                                                                                                                                                                                      1583 GAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAG 1642
                                                                                                                                                                                                                                                             1643 GAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGTCACTCGGGCTTCTACGAAAG 1702
                                                                                                                                                                                                                                                                                                                                                             1403 TGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGGTACAGGTGAAAGATGAT 1462
                                                                                                                               1463 GAATTAAGCCGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGATTGAT 1522
                                                                                                                                                                                                                                                                         1343 AGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAG 1402
                                                                                                                                          2003 ATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGAC 2041
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N.terminal or modified domains and constant demains, rod repeats, utrophin or a spectrin gene, H1 and H4 invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control comprol element, The dystrophin minigene in operable linkage with an expression useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human hinge H1 and rod R1), 8059-10227 (rods R22, R23 and R24, hinge H4 and cR domain) and ll047-11058 (dystrophin last 3 amino acids).
                                                                                                                                       New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1351 ACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTCTTGCCTGGCTTACA 1410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match
Local Similarity 100.0%; Pred. No. 5.6e-267;
nes 999; Conservative 0; Mismatches 0;
                                                                                                                                                                                                            Example 1; Page 50-51; 71pp; English.
   27-APR-2001; 2001WO-US13677.
                            28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 999; Conservative
                                                                                                               WPI; 2002-049342/06.
                                                         (XIAO/) XIAO X.
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1583 GAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACTGTACCAG 1642
            1643 GAGCCCAGAGAGCTGCCTCCTGAGGAGAGCCCAGAATGTCACTCGGGTTCTACGAAAG 1702
                                                        The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N\text{-}\mathsf{terminal} or modified
                                                                                         1703 CAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAG 1762
                                                                                                      1763 AGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTG 1822
                                                                                                                                                   1823 GACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTC 1882
                                                                                                                                                                                                                                 1883 CTCATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCG 1942
                                                                                                                                                                                                                                              1943 CCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGC 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adeno-associated virus vector plasmid, AAV-MCK-3531.
                                                                                                                                                                                                                                                                                                                             2003 ATTCAGGTCTCACGGTATAACCTCAGCACTCTGGAAGAC 2041
                                                                                                                                                                                                                                                                                                                                          2311 ATTCAGGTCTCACCGTATAACCTCAGCAGCTCTGGAAGAC 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 62-63; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                             AAD37258 standard; DNA; 4498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200183695-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD37258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xiao X;
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operable linked to an expression control element. The dystrophin minigene in operable linkage with an expression control useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (DMD) in a mammalian subject. The present sequence is AAV dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophy minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1703 CAGGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAACCTGCACTCCGCTGACTGGCAG 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1763 AGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTG 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1583 GAGACTGTACGAATATTTCTGACAGGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAG 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2648 GAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAACTCTACCAG 2707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1643 GAGCCCAGAGAGCTGCCTCATGAGAGAGAGCCCAGAATGTCACTCGGGTTCTACGAAAG 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1523 GTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTT 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1463 GAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAT 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1343 AGIGAACTICGGAAAAAGTCICICAACAITAGGICCCAITIGGAAGCCAGIICIGACCAG 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1403 TGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAACATGAT 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2468 TGGAAGCGTCTGCACCTTTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGAT 2527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1283 GAAGGTTCCGATGATGCAGTCCTGTTACAAGACGTTTGGATAACATGAACTTCAAGTGG 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1163 GACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAA 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2228 GACTCCAAGGGAGTAAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAATTTGAA 2287
                                                                                                                                                                                                                                                                                                                                                                                                                               1103 GAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGGTAAGGAAAGGCTCCTAGAA 1162
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                                                                                                                                                                                                                                                                    Length 4498;
                                                                                                                                                                                                                             Sequence 4498 BP; 1251 A; 1118 C; 1123 G; 1006 T; 0 other;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                            48.9%; Score 999; 25.7, 100.0%; Pred. No. 6.3e-267; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                        Score 999; DB 24;
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                            666
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The invention provides a gene for the treatment of muscular dystrophy having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                              A rod shortened dystrophin (deltaDysAH3) encoding nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                               1883 CTCATTGACTCTCCCAAGATCACCTCGAGAAGTCAAGGCACTTCGAGGAGAAATTGCG 1942
              1943 CCTCTGAAAGAAGAAGGTGAGGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGC 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A gene encoding a shortened dystrophin - useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune reaction. The present sequence represents a rod shortened
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 4402;
                                                                                                                                                                                                                                                                                                         Muscular dystrophy; rod domain; adeno-associated virus; AAV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4402 BP; 1339 A; 984 C; 1010 G; 1069 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.7%; Score 851.6; DB 21,
99.5%; Pred. No. 6.2e-226;
trive 0; Mismatches 4;
                                                                                                           2003 ATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGAC 2041
                                                                                                                         (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
                                                                                                                                                                                                       AAZ48568 standard; cDNA to mRNA; 4402 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 21-22; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                           dystrophin gene; truncated; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dystrophin encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0142134.
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                                                                                                                                                                                                                                                              31-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscular dystrophy
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                    JP11318467-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 854;
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        1335 CCAGTTTCATACTCATGAGGGGTACATGATGGGTTTTGACAGCCCATCAGGGCCGGGTTGG 1394
                                          1455 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGTAGC 1514
                                                                                                             1515 TAGCATGGAAAACAAAGCAATTTACATAGGTTTTAATGGATCTCCAGAATCAGAAACT 1574
                                                                                                                                              181 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                 241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATGAGAAGATGAAGA 300
                                                                                                                                                                                301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                    361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                 481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAAAATAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                     601 TGATGAATCTAGTGGAGATCAGGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGG 660
                                                                                                                                                                                                                                                                                                                                                       1935 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTT 1994
                                                                                                                                                                                                                                                                            661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACAT 720
                                                                                                                                                                                                                                                                                                            721 CCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 780
                                                                                                                                                                                                                                                                                                                                              781 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTAAAGGATCAAAATGAAATGTT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dystrophin; muscular dystrophy; probe; antibody; diagnosis; prenatal; heterozygote; gene therapy; genetic screening; foetal screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Partial sequence of murine muscular dystrophy (MD) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAN97129 standard; cDNA; 3275 BP.
                                                                                                                                                                                                                                                                                                                                                                                                1995 ATCAAGTCTCGAGAAGT 2012
                                                                                                                                                                                                                                                                                                                                                                                841 ATCAAGTCTTCAAAACT 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1992 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAN97129;
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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The inventors claim an MD probe comprising a purified ss NA SQ which hybridises to at least a part of the MD gene; pure dystrophin (DS) polypeptide, purified NA encoding DS and antibodies (Ab) to DS. The probes are equal to or greater than 10b of one of 12 cDNA sequences deposited as ATCC 58666-57677. The MD gene is human, or a murine Dmd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATGGTGGGTTCTTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TGCTGAGGACACATTGCAAGGACACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CCAGTTTCATACTCATGAGGGTACATGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATGAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCGAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAAGAAGAAAATGGAGGAAGA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAAAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 TGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGG 660
                                                                                                                                                             Muscular dystrophy gene – used for prepn. of probes, dystrophin polypeptide and antibodies for diagnosis and therapy of muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                             39.8%; Score 811.4; DB 10; Length 3275;
86.0%; Pred. No. 8.1e-215;
tive 0; Mismatches 146; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3275 BP; 1183 A; 606 C; 734 G; 752 T; 0 other;
                                                                                  Kunkel LM, Monaco A, Hoffman EP, Koenig M;
                                                                                                                                                                                                                       Example; Fig 7B; 68pp; English.
88WO-US04504.
                           87US-0136618.
                                                    (CHIL-) CHILDRENS MED CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                 WPI; 1989-220587/30.
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                P-PSDB; AAP93315
                        22-DEC-1987;
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CAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACAT 720
662 TTATGAATCCAGGGTGATCATGCAACAGCTGCTTTGGAAGAACAACTTAAGGTACTGGG 721
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661 AGATCGATGGCAAACAICIGIAGATGCCCAAACAICIGIAAAAAAAAAA		AGATCGATGGGCAAATATCTGCAGATGGACTGAAGACCCCC
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FEATURES
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                  US-09-845-416-2_COPY_960_3000
2041
                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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BI730168
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Gapop 10.0 , Gapext 1.0
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gb_est5:*
em_estfun:*
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em_esthum:*
em_estin:*
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em_estov:*
em_estpl:*
em_estro:*
em_estro:*
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gb_est2:*
gb_htc:*
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Score Match Length DB
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Maximum DB seq length: 5000
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                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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491.6
486.6
454.6
424.2
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B1250598 602993659 BF963618 QV2-NN004 AW467977 he29Q08.x B1259B102 UI-R-DKO-B153820 603190772 B158828 4012-24 M BEB17979 CM2-BN027 AK020881 Mus muscu AZ780314 2M018010 BQ375536 PM1-TN012 BQ375536 TL5-CT051 BE557463 f103h06 y	A226551 RPC1-23-9 B0244936 PM1-HT03-4 B02449936 PM1-HT03-4 B0212445 RST32032 B1289382 UI-R-DK0-18F72373 IL5-IT002 BF772375 IL5-IT002 BF772375 IL5-IT002 BF52118 UI-R-Y0-a AV704460 AV704460 B815203 PM0-BK013 AV30105 AV308105 A1789349 UK54a11. Y BJ075055 BJ075055 AV30165 AV30166 A	A1713038 UI-R-270-0 BQ379136 CM4-UT007 AV29496 CM4-UT007 AV29496 UI-M-BH3- BU61271 MR4-UT009 BM20473 C0269G08- BG077459 H3015F05- BM291527 EST578861 AQ260288 CITBL-E1- BB083824 BB083824 BG636373 SD14045.5 A1715599 UI-R-Y0-a	mRNA linear EST 20-SEP-2001 CDNA clone IMAGE:5357162 5', ata; Vertebrata; Euteleostomi; ognathi; Muridae; Murinae; Mus. alian Gene Collection (MGC) ttory G.E. Consortium (LLNL) Inc. Inc. ibution information can be ium/LLNL at:
13 B1250598 12 BF963618 10 AW467977 13 B1289102 13 B128920 13 B1988528 12 BE817979 11 AK020811 17 AZ780914 14 BQ375536 14 BQ319056 10 BE579463 10 BB651473		9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	834 bp m musculus 5864 Chordata; Crania Rodentia; Sciuro ici.nih.gov, of Health, Mamma usberg, ph.D. nih.gov The Cepko Laborat ation. Life Tech dby: The I. Life Tech dby: The I. M.A.C. E. Consortia M.A.C. E. Consortia W. e. column: 03 e stop: 796.
	2442087210877	4 4 4 4 4 4 4 W W W W W W W W W W W W W	BI729851 603349511F1 NIH_MGC_9 BI739851 BI729851.1 GI:157068 BEST. house mouse. Mus musculus ENERTYOLE: Rutheria: R 1 (Chases 1 to 834) NIH-WGC http://mgc.nc National Institutes of Onpublished (1999) Email: cgapbs-remail Tissue Procurement: Tissue Procurement: Tissue Procurement: Toba Library Preparal CDNA Library Preparal Library Musuality Sequence Location Qual
C C C C C C C C C C C C C C C C C C C		333 333 334 44 44 55	RESULT 1 B1729851 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT FEATURES SOUICE

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3,
                                  /clone_lib="NIH_MGC_94"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage_resistant)"
/note="Organ: eye, vector: pcMv-Spogre; site_1: Not1;
/note="Organ: eye, vector: pcMv-Spogre; site_1: Not1;
/note="Organ: eye, vector: pcMv-Spogre; site_1: Not1;
/note="Organ: eye, vector: pcMv-Spogre; site_2: Sali; Cloned unidirectionally; oligo-dT primed.

Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1605 CAGAGCAGCTITGGAAGGACTAGAGAAACTC-TACCAGGAGCCCAGAGAGCTGCCTCCT 1663
-643 CAGAGCAGCCTITGGAAGGACTAGAGAAACTCTTACCAGGAGCCCAGAGAACTGCTCCT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1664 GAGGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACT 1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1545 AATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGA 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1485 TIGGAGGCGACTICCAGCAGIICAGAAGCAGAACGAIGIACAIAGGGCCIICAAGAGGG 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1245 ACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCC 1304
                                                                                                                                                                                                                                                                                                                                                                                                                 1125 TCCTACAGGATGCTACCCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGC 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1185 TGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACA 1244
                                                                                                                                                                                                                                                                                                                                                 1065 TCCCCTGGACCTGGAAAGTTTCTTGCTGGTTACAGAAGCTGAAACAACTGCCAATG 1124
                                                                                                                                                                                                                                                                                   1005 ATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCACAGACTCATAGATTACTGCAACAGT 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                 123 TGATGAAACCATGGCAAGATGTCCCAAGGAGAATTGAAACTCACACAGATATCATGAAACTGAAAGATATCACA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 ATCTTGATGAAAATGGCCAAAAAATCCTGAGATCCCTGGAAGGTTCGGATGAAGCACCCC 342
                                                                                                                                                                                                                                                                                                                                                                    44 ATAAAAGAGTAAGTGAGGAAGAGGCTGCTTTGGAAGAAACTCATAGATTACTGCAGCAGT 103
                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                        DB 13; Length 834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1724 GAGTGGGAAAAATTGAACCTGCACTC-CGCTGACTGGCAGAGAAA 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.0%; Score 592.4; DB 13; Length 88.4%; Pred. No. 5.7e-130; tive 0; Mismatches 86; Indels
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5357162"
                                                                                                                                                                                                                                                                Matches 677; Conservative
                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                    Query Match
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BI730168 RESULT 2

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B1730168 750 bp mRNA linear EST 20-SEP-2001 603349711F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5357187 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="refina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye, Vector: pCWN-SPORT6; Site_1: Not1;
/note="Organ: eye, Vector: pCMN-SPORT6; Site_1: Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
full-length clones and constructed by Life Technologies.
this is a NIH_MGC Library.
a left c 178 g 170 t lothers
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                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1271 CIGAGAICCCIGGAAGGIICCGAIGAIGCAGICCIGTIACAAAGACGIITGGAIAACAIG 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1154 CTCCTAGAAGACTCCAAGGG--AGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAG 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1097 CITACAGAAGCIGAAAC--AACIGCCAAIGICCIACAGGAIGCIACCCG-IAAGGAAAGG 1153
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                                                                                                                                                                                                 NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                             Down Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Flate: LLAM11908 row: f column: 04
High quality sequence stop: 747.
High quality sequence stop: 747.
                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
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0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.1%; Score 491.6; Similarity 89.3%; Pred. No. 4.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:5357187"
                                                                                      BI730168.1 GI:15707181
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                                                         mRNA sequence.
                                                                                                                                house mouse.
                                                                      BI730168
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                                                                                                                                                                                                                    AUTHORS
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KEYWORDS
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
1451 CTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAG 1510
                                                                         1511 AAGCA-GAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAAT 1569
                                                                                                                                                  1570 CATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGA 1629
                                                                                                                                                                                                                       Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1200 AAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACA 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1260 GCCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTT 1319
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579 bp mRNA linear EST 25-FE
DKF2p762L078_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
AL715F2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
128 c 144 g 127 t
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23.8%; Score 486.6; DB 9; Length 579;
Best Local Similarity 97.2%; Pred. No. 7e-105;
Matches 495; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="DKFZp762L078"
/clone_lib="762 (synonym: hmel2)"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wiemann, S.
EST (Ottenwaelder, et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Ottenwaelder B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL121550.1 GI:5927551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999
                                                                                                                                                                                                                                                                                                  1690 GCTTCTACGA 1699
                                                                                                                                                                                                                                                                                                                                     740 GCTCCTACGA 749
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ACCESSION

KEYWORDS

REFERENCE AUTHORS JOURNAL

TITLE COMMENT

RESULT 3 AL121550

SASE COUNT

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HTC 12-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.systemsbiology.org
contact: amadanGsystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
                                            1320 TGGAIAACATGAACTICAAGIGGAGIGAACTICGGAAAAAGICICTCAACATTAGGTCCC 1379
                                                                                                                               1380 ATTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGG 1439
                                                                                                                                                                                                                   BC009242
Homo sapiens, dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272, clone IMAGE:3029414, mRNA
                                                                                                                                                                                                                                                                                                        1500 CAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAG 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                          1560 AACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGG 1619
131 GCCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTT 190
                                                                   cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1680 ATGTCACTCGGCTTCTACGAAAGCAGGCT 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC009242.1 GI:14714379
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pgm2n.pk007.117 Normalized Chicken Breast Muscle, Leg Muscle, and pgm2n.pk007.117 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk007.117 5' similar to sp[Pl1533|DMD_CHICK Dystrophin pir|S02041 dystrophin, muscle - chicken emb|CAA31746.1| (X13369) dystrophin (AA 1 - 3660) [Gallus gallus], mRNA sequence.
                                                                                                                                                                   0
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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                                                                                                                                                                                                                                                                                                                             121 TGCTGAGGACACATTGCAAGGACACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                            181 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 TAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                  1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                     0; Gaps
                                                                                                                                      DB 11; Length 1490;
                                                                                                                                                                       4; Indels
                       /tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.3%; Score 454.6; DB 11
99.1%; Pred. No. 3.6e-97;
Live 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cogburn, L.A. and Monsonego-Ornan, E.
             /clone="IMAGE:3029414"
                                                        /lab_host="DH10B-R"
/note="Vector: pOTB7"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
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                                                                                                                                                                            Matches 457; Conservative
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                                                                                                                                                            Similarity
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/dev_stage="Breast,leg:Embryo(d19):post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(l1,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                          /note="vector: pcMvSPORT6; Library made from equivalent /note="vector: pcMvSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic pools of total RNA isolated 33.3%; and epiphyseal growth muscle 33.3%; juvenile muscle 33.3%; of the final RNA pool). Single pass sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1663 TGAGGAGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATAC 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1723 TGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAAAAATAGATGAGACCCT 1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1603 GACAGAGCAGCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCC 1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1483 TATIGGAGGCGACTITCCAGCAGTICAGAAGCAGAACGAIGIACAIAGGGCCTICAAGAG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1543 GGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCT 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1423 TCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGACC 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1303 CCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTC 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1363 TCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACTTTC 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Commercial broiler and Ottawa Res. Centre Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TCTAAACATTAGATCTCATTTGGAAGCCAGCACAGAGCATGGAAGCGTTAACATCTCTC
                                                                                                                      /clone="pgm2n.pk007.117"
/clone_lib="Normalized Chicken Breast Muscle, Leand Epiphyseal Growth Plate cDNA library (pgm2n)
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 424.2; DB 13; Length 663;
Pred. No. 4.8e-90;
0; Mismatches 144; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                           6 others
Email: cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                                                                                                                             172 g 144 t
                                                         /organism="Gallus gallus"
                                                                                                              /db_xref="taxon:9031"
                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             from 5'-end"
132 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.8%;
78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 518; Conservative
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BI250598.1 GI:14799101
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BI250598
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                                                                                               BC011062 2334 bp mRNA linear HTC 07-AUG-2002
Mus musculus, Similar to utrophin, clone IMAGE:3979320, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                       Submitted (25-Jul-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     through the I.M.A.G.E. Consortium/LIND at: http://image.llnl.gov
Series: IRAK plate: 23 Row: j Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein
This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam1" mouse. Taken by biopsy." /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 AGTICATIGAIGGAGAGIGAAGIAAACCIGGACGITATGAAACAGGITIAGAAGAAGTA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 TTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAATGAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.3e-70;
0; Mismatches 410; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 GTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCC 223
                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BNA Sequencing Center
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.8%; Score 343; DB 11; Length 2334; 59.0%; Pred. No. 1.3e-70;
                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6" 512 c 638 g 486 t
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                                                                                                                                         BC011062.1 GI:15029695
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602993659F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5149431 5'
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 772)
                                                                                                                                344 GAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGAT 403
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue preparation: Li.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://inage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 265.8; DB 13; Length 772;
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0; Mismatches 287; Indels
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:5149431"
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                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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High quality sequence stop: 771.
Location/Qualifiers
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61.4%;
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/organs="Homo sapiens"
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/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_l: Smal;
/note="Organ: nervous_normal; Vector: puc18; Site_l: Smal;
/note="Organ: nervous_normal; Vector: puc18; Site_l: Smal;
/note="Organ: nervous_normal; Vector: Reverse transcription
derived from ORBSTES PCR (U.S. Letters Patent application
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No. 196,716 - Ludwig Institute for Cancer Research
No. 196,716 - Ludwig Institute for Cancer Research
Issue mRNA and cDNA amplification were performed under
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low stringency conditions.

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This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2.NNO045-
211200-570-d02&t3=2000-12-21&t4=1)
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Mammalia; Eutheria Primates; Catarrhin; Hominidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Sllvay, Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Goldman,G.H., Geoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 22-JAN-2001
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF963618
QV2-NN0045-211200-570-d02 NN0045 Homo sapiens cDNA, mRNA sequence.
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                                                   644 CAACTTAAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACGCTGG 703
565 CACATGGTGGTGATTGTGGATGAAAACAGTGGGGAGAGTGCCACAGCTCTTCTGGAAGAT 624
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                                                                                                                                                                                                                                                                                               AW46/977 645 bp mRNA linear EST 24-FEB-2000 similar to SW:UTRO_HUMAN P46939 UTROPHIN; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs r@mail.nlb.gov
Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
Genome Sequencing Center
Clone Sistribution: NCI-CGAP clone distribution information can be
www-bio.lln.gov/bbrp/image/image.html
High Amailty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:2920478"
/clone_lib="NCI_CGAP_CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and /lab_host="bH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 645)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                1117 TGCCAATGTCCTACAGGATGCTACCGGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGT 1176
                                                                                                 1177 AAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGT 1236
                                                  /note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: Sali; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."
                                                                                                                     5 GCAACAGIICCCCCIGGACCIGGAAAAGIIICIIGCCIGGCIIACAGAAGCIGAAACAAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1082 AAGITICIIGCCIGGCITACAGAAGCIGAAACAACTGCCAAIGTCCIACAGGAIGCIACC 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1142 CGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAA 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1202 GACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGC 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               645 AACTICCTGAAGTGGATCCAAGAAGGAGACCACAGTGAATGTGCTTGTGNATGCCTCT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585 CATCGGGAGAATGCTCTTCAGGATAGTATCTTGGCCAGGGAACTCAAACAGCAGATGCAG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 645;
                                                                                                                                                                  1237 TTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCTG 1282
                                                                                                                                                                                      0; Mismatches 272; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3e - 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9%; Score 182.4;
56.4%; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Best Local S
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                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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linear EST 19-JUL-2001
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The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first tail. The sequence tag present in the cDNA backen the Notified poly A and the oligo-dT track served to identify it as a clone from the normalized rat placenta pool library CDNA Library Preparation. W.B. Research Genetics (www.resgen.com) The following repetitive elements were found in this CDNA sequence: 1-21,
                                                                           1262 CAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTG 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                   1322 GATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAGGTCTCTCAACATTAGGTCCCAT 1381
465 CAGAAGATGGTAAAAGCTTTGGGAAATTCTGAAGAGGTACTATGCTTCAACATGGACTG 406
                                                                                                                                                                                                                                                                                        1382 TIGGAAGCCAGIICIGACCAGIGGAAGCGICIGCACCIIICCIGCAGGAACIICIGGIG 1441
                                                                                                                                                                                                                                                                                                                                                                                             1442 TGGCTACAGCTGAAAGATGAATTAAGCCGGCAGGACCTATTGGAGGCGACTTTCCA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1502 GCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAA 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                     405 GATGATGAACCAAAGATGGAATGACTTAAAAGCAAAATCTGCTAGCATCAGGGCCCAT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1562 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGGAGCCTTT---- 1617
                                                                                                                                                                                                                                                                                                                       1618 -----GGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAG 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI289102
UI-R-DKO-cfe-e-07-0-UI.S1 UI-R-DKO Rattus norvegicus CDNA clone
UI-R-DKO-cfe-e-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            285 TGGCTGAATATGAAAGATGAAGAGCTTAAGAAACAAATGCCTATTGGAGGAGATGTTCCA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 GCCTTACAGCTCCAGTATGACATTGTAAGGCCCTGAGACGAGTTAAAAGAGAGAAAAGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 TATTCTGTCCTGAATGCTGTCGACCAGGCCCGAGTTTTCTTGGCTGATCAGCCAATTGAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 GCCCCTGAAGAGCCAAGAAAGCTACAATCAAAAACAGAATTAACTCCCTGAGGAGAGA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1673 GCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTC 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 GCCCAAAGGTTGCCAAGCCATGCGCAAACAGTCTTCTGAAGTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
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BI289102.1 GI:14946326
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                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZUU. (EXCEPTION: The aorta pool does not contain emulyouic day 17 RNA and the placenta pool contains only the three embryonic stages). Each library was normalized embryonic stages. Each library was normalized by individually according to the procedure described by anomalo, 1996, 1996. For construction of the DKO subtracted libraries (Genome Research Genome 6: 791-806, 1996). For construction of the procedure described by tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries circular DNA representing these five normalized libraries with a driver (PCR amplified inserts from a plasmid DNA with a driver (PCR amplified inserts from a plasmid DNA temptate preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five nor-normalized libraries of brain (CTOS), heart (CSOS). Kidney (CUOS), libraries of brain (CTOS), heart (CSOS). Kidney (CUOS) approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTOS), heart (CSOS), and placenta (CXOS). The resulting pool of a placenta (CXOS). The resulting pool of a placenta (CXOS). The final driver population.
                                                                                                                                                                                                                                                                                      /idu_incst_ units (line identical) with a modified force="Vector: pT73D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DKO polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DKO polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DKO polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DKO polylinger of two mixture of five individually tagged normalized rat libraries: hart-nRAP (20%), heart-nRAP (20%), heart-nRAP (20%), and placenta-nRAP (20%). Each original actra-nRAP (20%), and placenta emixture of equal amounts of library was constructed from a mixture of equal amounts of library was constructed from a mixture of equal amounts of embryonic day 17, adult day 19, embryonic day 21, adult day 12, adult day 75, and adult day 200. Exception: the actra pool does not contain embryonic contain embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497 CTTGAAGACCTAAAACGCCAAGTACAACATAAGGTGCTTCAAGAAGATCTAGAACAA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 CTACCCTCCTGCAAAACCTGCTTGAAGAACATAAAAGTTTGCAAAGTGACCTCGAAGCT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 TGGCTGACCTCACAGAGGAGGGCATTCAGAAGATGGAAAGCCTCCCAGTGGGTGACGAC 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             579 CAGATGACCTTGCTGAACGCCAGATGGGAGGCGCTCCGGGTAGAGAGCATGGAGAGACAG 520
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                                                                                                                                                                     /clone_ilb="UI_R-DK0-cfe-e-07-0-UI"
/clone_lb="UI_R-DK0"
/dev_stage="ADULT"
/lab_nost="DHIOB_(Life_Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_LIB-UI-R-DKO
TAG_TISSUE-rat placenta pool
TAG_SEQ-TCACGACAGT"
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                                                                   /organism="Rattus norvegicus"
                                                                                                         /strain="Sprague-Dawley/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 g
Location/Qualifiers
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                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Fissue Procurement: Miklos Palkovits, M.D., Ph.D.

FonA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Preparation: Michael J.

FonA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: Thocyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo. (bases 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1457 GATGATGAATTAAGCCGGCAGGACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAG 1516
                                                                                                                                                                                                                                                                                                                                                                       603190772F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262209 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                             677 ATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAA 736
                                                                                                                                                                                    219 GTATGCCGCTGGACTGAAGAACGTTGGAACAGGTTGCAAGAAATCAATATTTGTGGCAG 160
                     617 GATCACGCAACTGCTTGTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGCAAAC 676
557 GAACAAGTCAGGGTCAATTCTCTCACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.5%; Score 172.8; DB 13; Length 835; 56.0%; Pred. No. 2.7e-30; Live 0; Mismatches 257; Indels 0;
                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM11660 row: p column: 18
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                                                                                                                                                                                                                                                                                                                                                                   835 bp
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BI553820
BI553820.1 GI:15441132
                                                                                                                                                                                                                                      737 CGICITACIGAAGAACAG 754
                                                                                                                                                                                                                                                                            159 GAATTATTGGAAGAACAG 142
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Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H. Gene expression in the developing mouse retina by EST sequencing and microarray analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4012-24 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA,
1517 AACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGT 1576
                                                                                                            1577 ACTCTTGAGACTGTACGAATATTTCTGACAGGCCAGCCTTTGGAAGGACTAGAGAACTC 1636
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/dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps (Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
                                                                                                                                                                                                                           1637 TACCAGGAGCCCAGAGGTGCCTCCTGAGGAGAGAGCCCAGAATGTCACTCGGCTTCTA 1696
                                                                                                                                                                                                                                                                                                                                       1697 CGAAAAGCAGGCTGAGGGGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGAC 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1757 TGGCAGAGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGAT 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1817 GAGTIGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGC 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1877 GATCICCICAITGACICICCCAAGAICACCICGAGAAAGICAAGGCACIICGAGGAGAA 1936
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                                 126 GTGCTGGAGTCAGGCCTTCCTGTCCAGCACCATTGAGGAGTTAGAGGAGCCT 185
                                                                                                                                                                                                                                                               186 CATICIGAGAGCAAAGATACCTCCCCGAAACAGCGGATCCAGAAATCTCAGCCGTTTGTA 245
                                                                                                                                                                                                                                                                                                                                                                           246 TGGAAGCGACGGTGGCCAGTGAACTGTGGAAAGTTGACAGCCGCTGTGGAAC 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 Trotococoargaaagarggagraaagrrggrgaargarcrggcccaccaacrrgccarr 545
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/clone_lib="Mouse E14.5 retina lambda 2AP II Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA Fax: 713 790 0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997 ITGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGA 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 TATGATGTGCACTTGTCAATGGAGAATTCCCAGGCCCTGGAACA 589
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DEFINITION RESULT 12 BI988528

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REFERENCE AUTHORS MEDLINE

COMMENT

FEATURES

JOURNAL

TITLE

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Insertion site: TACGTCCACTGAATTCTGAGGG--->. Other information regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_libraries.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 bp mRNA linear EST 21-SEP-2000 CM2-BN0275-070600-221-a02 BN0275 Homo sapiens cDNA, mRNA sequence. BE817979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neco, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fmail: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM2-BN0275-070
600-221-a02&t3=2000-06-07&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                         1005 ATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCACAGACTCATAGATTACTGCAACAGT 1064
                                                                                                                                                                                                                                                                                                                                                1065 TCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACAGAAGAAGAACAACTGCCAATG 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                         1125 TCCTACAGGATGCTACCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGC 1184
                                                                                                                                                                                                                                                                                                                                                                          367 ATAAAAGAGTAAGTGAGCAAGAGGCTGCTTTGGAAGAAACTCATAGATTACTGCAGCAGT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1185 IGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTT 1238
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                        43; Indels
                                                                                                                                                                     8.1%; Score 165.2; DB 1
31.6%; Pred. No. 1.5e-28;
                                                                                                            119 t
                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 427.
Location/Qualifiers
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                                                                                                                                                                                                         Matches 191; Conservative
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and Subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930021A21:utrophin, full insert sequence.
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  707 CITITACAAGACAICCITCICAAAIGGCAACGICIIACIGAAGAACAGIGCCITITIAGI 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 AIGGIGGICATIGITGAIGAAAACAGIGGIGAGAGIGCIACAACCIAICCIAGAAGACCAG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 CTTAAGGTATTGGGAGATCGATGGCCAAACATCTGTAGATGGACAGAAGACCGCTGGGTT 706
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                                                                                                                                                                                                                                                                                                                                                                                                                       426 CAGAAGAAGCAACTGCAGCAGCTCTCCGCCTGGTTAACACTCACAGAGGAGGGCGCATTCAG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 AAAATGGAGGAAGACCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 AAGATGGAAACTTGCCCCTGGATGATGTGAAAATCTCTACAAAAGCTGCTAGAAGAA 307
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                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (strain:C57BL/6J) adult retina cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                         Query Match 7.9%; Score 162; DB 12; Length 427; Best Local Similarity 61.3%; Pred. No. 8.1e-28; Matches 261; Conservative 0; Mismatches 165; Indels
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S Adachi, J. Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Koya, S., Kato, H., Kawai, J., Kolima, T., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, R., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tanaka, T., Yamamura, T., Yamamura, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-AGG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Genomic Sciences Center (GSC), RIKEN Group, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                          Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Ailyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwaqi,K., Yoneda,Y., Ishikawa,T., Ogawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inouc,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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1609 GCAGCCTTTGGAAGGACTAGAGAAAC 1634
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                               with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI. Host: DHIOB. Retina RNA was provided by Stefano Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged.
                             cDNA was cleaved
                                                                                                                                  Retina RNA was provided by Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged.
                                                                                                                                                                                                                                                                                                                              /tissue_type="retina"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .885
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ASIRAHLEASAEKWNRLLASLEELIKWLNMKDBELKKOMPIGGDVPALQLQYDHCKVL
RRELKEKEYSVLNAVDQARVFLADQPIEAPEEPRRNPQSKTGERGSFL"
190 c 235 g 214 t
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              0; Mismatches 183; Indels
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Pred. No. 1.2e-25;
                                                                                                                                                                                                                                                                         /db_xref="MGD:MGI:1911691"
/db_xref="taxon:10090"
/clone="A930021A21"
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                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAB32239.1"
/db_xref="G1:12861603"
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                               /strain="C57BL/6J"
adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Utrn"
259. .885
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/gene="Utrn"
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59.0%;
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Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclocided kinase. Adaptor oligoucleotides were adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114pl/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors
                                                                                                                                             GSS 16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                             AZ780914 16 515 bp DNA linear GSS 16-FEB-200
2M0018010R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 10000 Std Error: 0
Plate: 0018 row: 0 column: 10
Seq primer: CACACAGGAAACAGCTATGACC
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 515.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
810 TCAGCCAATAGAGGCCCCCGAAGAAC 835
                                                                                                                                                                                                                                AZ780914.1 GI:12913077
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801 585 7177
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Search completed: April 25, 2003, 17:37:33 Job time : 1947.12 secs

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Sequence 3, Appli
Patent No. 5180810
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-910-372-4
US-08-91-527-212
US-08-847-534A-22
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US-09-385-982-236
US-08-30-915A-193
US-08-139-937-12
PCT-US93-11310-12
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                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                            468 AAATGGAGGAAGAGCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAC 527
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Ouery Match 2.0%; Score 40.4; DB 1; Length 2223; Best Local Similarity 51.7%; Pred. No. 0.06; Matches 92; Conservative 0; Mismatches 86; Indels 0;
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44.0%; Pred. No. 0.2;
tive 0; Mismatches 209; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Birch, Stewart, Kolasch & Birch
: 301 No. 5728810th Washington Street
Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08425069
Patent No. 5728810
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hinmen, Michael B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MUTDHY JI., GETALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 114.
TELECOMMUNICATION INFORMATION:
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TELEFAX: (703) 205-8050
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TYPE: nucleic acid
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APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND PRODUCTS THEREOF
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                           971 TAGGAGGTTATGGACCAGGACAACAAGGTCCAGGAGATATGGACCAGGACAAGAAGGTC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1802 CAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCCCAAGCTGAGGTGATCAAGGGATCC 1861
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                                                                                                                                                                                                                                                                            1682 GTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAAC 1741
                                                                                                                                                                                                                                                                                                                                                                    1742 CTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTT 1801
                                                                                                                                                                                  1622 GGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAAT 1681
1502 GCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAA 1561
                                                                                          1562 CCTGTAATCAIGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA 1621
                                                                                                                                                                                                                                                                                                                      911 GACCATCIGGAGCAGCAGCAGCAGCAGCAGCAGCAGGACCTGGACAACAAGGAT 970
                                                                                                                       731 GCAGTGCAGCTGCAGCAGCAGCAGCAGCACCTGGACAACAAGAACCGGAGGATATGGAC 790
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APPLICATION NUMBER: US/08/317.844P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Birch, Stewart, Kolasch & Birch
: 301 No. 5989994th Washington Street
Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703) 241-1300
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                                                                                                                                                                                                                                        731 GCAGTGCAGCTGCAGCAGCAGCAGCACCTGGACAACAAGAACCGGGAGGATATGGAC 790
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45.9%; Pred. No. 0.18;
itive 0; Mismatches 153; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gomi, Hideyuki; Hozumi, Tatsunobu; Hattori, Shizuo; Tagawa, Chiaki; Kishimoto, Fumitaka; Bjorck, Lars TITLE OF INVENTION: PROTEIN H CAPABLE OF BINDING TO IGG NUMBER OF SEQUENCES: 4 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/376,641
FILING DATE: 07-JUL-1989
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Matches 130; Conservative
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                                                                            1..1785
IMMEDIATE SOURCE:
                                                      NAME/KEY: CDS
LOCATION: 1..1
                CLONE: p6B
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                                                                                    US-08-317-844B-3
                                                                                                                                                                164;
                                                                                                                              Query Match
                                  FEATURE:
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Sequence 447, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn boucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACLD AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PLING DATE: 1997-11-08
PRIOR PLING DATE: 1997-08-14
PRIOR PLING DATE: 1997-08-14
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45.9%; Pred. No. 0.24;
ive 0; Mismatches 153; Indels 0,
                                                                                                                                                APPLICANT: Gomi, Hideyuki; Hozumi, Tatsunobu; Hattori, Shizuo; Tagawa, Chiaki; Kishimoto, Fumitaka; Bjorck, Lars TITLE OF INVENTION: PROTEIN H CAPABLE OF BINDING TO IGG NUMBER OF SEQUENCES: 4 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/376,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.9%; Score 38.2; DB 4; Length 1848;
48.0%; Pred. No. 0.25;
tive 0; Mismatches 118; Indels 0
521 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAG 563
                                    397 TTAGAACGTAAATACCAACGAGAAGTAGAAAAACGTTATCAAG 439
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CRGANISM: Staphylococcus epidermidis
US-09-134-001C-447
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Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                      5180810
                                                                                                                                                                                                                                                                                                           LENGTH: 1784
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                                                                                                                                    ; Patent No.
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                                                                                                                                              327 TGAAAGTTTAGAAGAGTTCTTCAAATAGTAGGGAATATTCATATCAACATTTCAAA 386
207 AGTTGAAATTTTCTCAATAATCACCTTTTATCGTTAAAAGTAGCGCGAAAAGTGCCTT 266
                                        853 AAAACTGGCCGTTTTAAAAGCGGATCTAGAAAAGAAAAAGCAATCCATGGGCAAACTGTA 912
                                                                              913 TTCACTCAAACAAGATCTTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAGACGGA 972
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                                                                                                                                                                                                      973 AGCATGGCTGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAA 1019
                                                                                                                                                                                                                               APPLICANT: Dundas Milne Edwards, Jean-Baptiste APPLICANT: Dundas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Complementary DNAS FILE REFERENCE: GRNST. 021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/247,155A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1999-02-09
CURRENT FILING DATE: 1999-02-09
EARLIER PELING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER PELING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER PELING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: Von Heijne matrix
INFORMATION: SCORE 5.9
INFORMATION: SEQ LTLLGLSLILAGL/IV
                                                                                                                                                                                                                                                                                                                                                  Sequence 76, Application US/09247155A Patent No. 6312922
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ORGANISM: Homo sapiens
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LOCATION: 46..87
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Best Local Similarity
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LOCATION: 1382..1394
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                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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1667 ITAATCAAAIGTAAACATAIGTTITCTAACACCAGTATAGAAAATACAAAACTAATTACA 1608
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48.4%; Pred. No. 0.47;
ive 0; Mismatches 111; Indels 0;
                                              APPLICANT: Hillman, Jennifer L.
APPLICANT: Tue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1607 ATCAGAACAATTTCTACCTTATCCTACTATAGTAA 1573
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                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/985,335 FILING DATE: Filed Herewith
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; Patent No. 6281334
; GENERAL INFORMATION:
Sequence 4, Application US/08985335 Patent No. 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.8%;
Best Local Similarity 48.4%;
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: Filed He PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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1352286
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LIBRARY: LATRI
                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                94304
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APPLICANT:

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SEQ ID NO:1:
: LENGTH: 1886
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US-08-961-527-212
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Patent No. 6420135
GENEAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
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48.4%; Pred. No. 0.47;
tive 0; Mismatches 111; Indels 0
                                                                                                                          APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL.
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
Hillman, Jennifer L.
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NAME: Billings, Lucy J.
REGISTRATION UNDBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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IBM Compatible
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Lal, Preeti
Shah, Purvi
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Best Local Similarity 48.4%
Matches 104; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; IMMEDIATE SOURCE:
; LIBRARY: LATRIUT02
; CLONE: 1352286
US-09-410-372-4
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                                                                                       APPLICANT:
APPLICANT:
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                               APPLICANT
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671 GCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACATCCTTCTCAAA 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 45.5%; Pred. No. 0.68;
Matches 131; Conservative 0; Mismatches 157; Indels 0;
                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPOTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text CURREWT APPLICATION DATA: APPLICATION NUMBER: US/08/961,527
                         ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/270,099
FILLING DATE: 14-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 186,097
FILING DATE: 25-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340
TELECOMMUNICATION INFORMATION:
TELEFAN: (301) 309-8514
INFORMATION FOR SEQ ID NO: 212:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 3902 base pairs
CORRESPONDENCE ADDRESS:
                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Query Match
1.8%; Score 36.6; DB 4; Length 1845;
Best Local Similarity 48.0%; Pred. No. 0.77;
Matches 135; Conservative 0; Mismatches 144; Indels 2; Gaps
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                                                                                                                                                                                                                                                                                454 AGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACG 513
                                                                                                                                                                                                                                                                                                                           394 TITAAIGGAICICCAGAAICAGAAACIGAAAGAGIIGAAIGAGIGGCIAACAAAAAACAGA 453
                                                                                                                                        321 AGAACGTGAAAAATATCTATGTTATGCTGACGATAAAGAAAAAAAGATCCTCAATCTAGAGC 380
                                          261 AGCGTGGAACTGGCCTAAAGAATATAACGCGTTACTTAAGGAAAATGAGGAGGTCAAGGT 320
                                                                                          334 ITCAAGAIGGGAAIGCCICAGGGIAGCIAGCAIGGAAAAACAAAGCAAITIACAIAGAGI 393
274 AACAGGAAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GAPPLICANT: Holden, David W.
APPLICANT: Holden, DAVID NATI-BACTERIAL METHODS AND MATERIALS
TITLE OF INVENTION: 106
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
CORRESPONDENCE MATSHAIL, O'Toole, Gerstein, Murray & Borun ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                514 CCAAGTACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACA 561
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,534A
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DESCRIPTION: /desc = "DNA (genomic) (p14c15)"
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COUNTRY: United States of America
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08887534A Patent No. 6455323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28341
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
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CLASSIFICATION: 536
ATTORNEX/AGENT INFORMATION:
NAME: AID-LAUCES, LI-HSIEN
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
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LOCATION: 856..1842
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123 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 182
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                                                                                                                                                           469 AAATCGTCAACTTGGATGGGCTACAACTATCCTTCACGATTAAAGATAGTGATTTTCATC 528
                                                                                                                                                                                                                                                                           529 AAATTICTATGATTCTT - GAAACATTAAAGAATCAATATGAAGCATTAGCTTATAAAAT 586
                                                                                                   210 TGGATITGACAGCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGA 269
                                      349 TGGCTTTGGATAAACATATGATGCATGTAACAATTAGTTATCCCCTACCTGACAATCAGC 408
                                                                              270 TIGGAACAGGAAATTAICAGAAGATGAAGAACIGAAGTACAAGAGCAGATGAATCTCC 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liu, Rihe TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                            450 CAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGA 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION UNBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 60/035,963 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06 NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17 LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09007005B Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 6.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL SZOSTAK, JACK W.
APPLICANT: SZOSTAK, JACK W.
APPLICANT: ROBERTS, Richard
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342 GGGAATGCCTCAGGGTAGCTAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATGG 401
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APPLICANT: Sociata, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Roberts, Richard W.
APPLICANT: APPLICANT: ROBERTS, RICHARD W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 00786/350007
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE FALSKEY FALSKEY FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 36.2; DB 4; Length 289;
Best Local Similarity 6.1%; Pred. No. 0.3;
Matches 14; Conservative 99; Mismatches 118; Indels
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APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Racie, Lisa A.
APPLICANT: Treacy, David
APPLICANT: Spaulding, Vikin
APPLICANT: Apostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: 32
CORRESPONDENCE: 32
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Translation template
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                                              Sequence 17, Application US/09244796 Patent No. 6281344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09014969
Patent No. 5965397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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RESULT 14
US-09-244-796-17
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ENGTH: 289
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244 TATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAAC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 AGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 36.2; DB 2; Length 2447;
Best Local Similarity 46.8%; Pred. No. 1.2;
Matches 110; Conservative 1; Mismatches 124; Indels 0;
                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 25, 2003, 17:42:33
                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Springer, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 498-8284
INFORMATION FOR SEQ ID NO:
SQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
US-09-014-969-14
Cambridge
                                  U.S.A.
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                                COUNTRY:
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

April 25, 2003, 17:39:49 ; Search time 135.61 Seconds Run on:

(without alignments)
16376.941 Million cell updates/sec

US-09-845-416-2_COPY_960_3000 2041 Perfect score:

1 tccttcacagcatttggaag.....acctcagcactctggaagac 2041 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

709820 seqs, 544064369 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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/ Ggn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/ Ggn2_6/ptodata/1/pubpna/U808_NEW_PUB.seq:*
/ Ggn2_6/ptodata/1/pubpna/U808_NEW_PUB.seq:* Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		•	Sequence 15766, A	Sequence 6092, Ap	Sequence 11083, A		20070	322/2/	Sequence 10/42, A	Sequence 18355, A	Seguence 4010. An	207	100	Sequence 12395, A	Sequence 343, App	Sequence 183, App	Segmence 183 App	100	seduence 183, App	Sequence 183, April	0	, cor	Sequence 183, App	Sequence 183, App	
B ID	10 113-09-864-761-01066	10 115-00-064 161 151-01936	10 da-09-004-/01-15/66		10 05-09-864-761-11083	10 US-09-864-761-27715	10 US-09-864-761-32272	10 US-09-960-352-10742	24/0T #26 00 50 51 U	CC 97 - 107 - 10333	US-09-960-352-4010	10 US-09-864-864-204	10 US-09-960-352-12395	TIC-00-000-040	72 10 12 12 12 12 1		9 US-10-176-758-183	HS-10-175-737-193	107 07 07 07		US-10-175-738-183	115-10-175-750-100	T-70/	US-10-176-482-183	
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	eouenbec	Sequence	Segmence	1000	eduence	Sednence	Segmence	00000000	acdueince.	Sednence	Sednence	Seguence	Sequence	Segmence	opion Engl	and and and a	actions	eduence	Sednence	Sednence	Sequence	Sequence	Segmente	Codemoes	הלתבווכם	Sednence	Sequence	Seguence	Sections	Seguence
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3-10-176-7	1.	-0/1-01	-10-1	-10-180-	0 1	-10-1/3-	-10-174-	-10-174-	-10-174-	10-17	10-1/4-	፣ '	-10-175-	-10 - 17	-10 - 17	-10 - 176 -	-10-176-	-10-176-	100	10.1.01	-9/T-OT-	-10-176-	-10 - 17	-10-176-	-10-104-	10 101	9-8/T-0T	-10-173-	-10 - 173 -	10-174-
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ALIGNMENTS

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                       HILLE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-24
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-39
PRIOR FILING DATE: 2000-06-39
PRIOR FILING DATE: 2000-06-39
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                          Sequence 21956, Application US/09864761
Patent No. US20020048763A1
                                                                                                                           GENERAL INFORMATION:
US-09-864-761-21956
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wesheng
TITLE OF INVENTION: HUBBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       983 GATAACITTGCCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACACCACAG 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 GITTIAAAAGCGGAICTAGAAAAGAAAAAGCAAICCAIGGGCAAACIGIATICACICAAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO AC004468.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.41
US-09-864-761-15766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%; Pred. No. 4.76
Matches 180; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6092, Application US/09864761
Patent No. US20020048763A1
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ORGANISM: Homo sapiens
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Best Local S
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 CATTIGGAAGCICCIGAAGACAAGICATITGGCAGITCATIGAIGGAGAGIGAAGIAAAC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.3%; Score 190.2; DB 10; Length 256; 98.5%; Pred. No. 3.3e-45; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN UUNG, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: SXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: WISSPROT HIT: 911532, EVALUE 2.00e-30
US-09-864-761-21956
             PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ACTCATGAGGTAAAC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Chen, Wensheng TITLE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

Hanzel, David K.

APPLICANT:

CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456

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Query Match

8.7%; Score 177; DB 10; Length 466;
Best Local Similarity 100.0%; Pred. No. 3.5e-41;
Matches 177; Conservative 0; Mismatches 0; Indels
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INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00601
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                         PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PELING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00667
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                PRIOR APPLICATION NUMBER: GB 24263.6
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OTHER INFORMATION: EXPRESSED IN PLACY
OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN HEARY
OTHER INFORMATION: EXPRESSED IN BRAIT
OTHER INFORMATION: EXPRESSED IN BRAIT
PRIOR FILING DATE: 2000-08-03
                                                                              DATE: 2000-10-04
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ORGANISM: Homo sapiens
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SEQ ID NO 6092
LENGTH: 466
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PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PELING DATE: 2000-05-26

PRIOR PLING DATE: 2000-06-03

PRIOR PELING DATE: 2000-01-04

PRIOR PELING DATE: 2000-01-04

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2000-09-21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 99.4%; Pred. No. 2.6e-34;
Matches 154; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                     CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
CTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 0.84
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96
CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88
US-09-864-761-11083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499 TGAAGACCTAAAACGCCAAGTACAACAACATAAGG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AC004468.1
                                       TYPE: DNA
ORGANISM: Homo sapiens
SEQ ID NO 11083
LENGTH: 467
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68 AACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTGTGCTGAG 127

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128 GACACATTGCAAGCACAAAGAGATTTCTAATGATGTGGAAGTGGTGAAAGACCAG 184

Sequence 11083, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.

JS-09-864-761-11083

RESULT 4

8 CAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAGTGAAGTA 67

0; Gaps

Annomax Sequence Listing Engine vers. 1.1

NUMBER OF SEQ ID NOS: 49117 SOFTWARE: Annomax Sequence

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0; Gaps

0; Indels

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenshengh K.
APPLICANT: Chen, Wenshengh E.
APPLICANT: HUANN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                     442 AACAAAAACAGAAGAAAGAAGAAAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGA 501
                                    382 ILTACAFAGAGITTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCT 441
                                                                   NUMBER OF SEO ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
0; Mismatches
                                                                                                                                                                                                                                                                                 502 AGACCTAAAACGCCAAGTACAACAACATAAG 532
                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Acomica.X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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Patent No. US20020048763A1
      Matches 151; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.4%; Score 151; DB 10; Length 151; Best Local Similarity 100.0%; Pred. No. 6.2e-34;
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82

OTHER INFORMATION: EXPRESSED IN LUGK, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN LUGK, SIGNAL = 0.84

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81

OTHER INFORMATION: WHIST MI8533.1, EVALUE 6.00e-80

OTHER INFORMATION: SWISSPROT HIT: P11532, EVALUE 4.00e-08
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                              433 TGAAGACCTAAAACGCCAAGTACAACAACATAAGG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNDBER: PCT/US01/00670
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 99/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR PLING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-36 PRIOR FILING DATE: 2000-08-03 PRIOR PILING DATE: 2000-08-03 PRIOR FILING DATE: 2000-10-04 PRIOR FILING DATE: 2000-10-04 PRIOR FILING DATE: 2000-10-07
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PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00665
PRIOR PLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
                                                                                                                                                                               Sequence 27715, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                     APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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LENGTH: 151
                                                                                                                                                            US-09-864-761-27715
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OTHER INFORMATION:

; OTHER INFORMATIC US-09-864-761-32272

OTHER

Similarity

Query Match

Best Local

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RESULT 7

1041 AG 1042

121 AG 122

q δ

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 AGGAAAATTAICAGAAGAIGAAGAAACTGAAGIACAAGAGCA--GAIGAAICICCIAAAI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 423;
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OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN HBLA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
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2.1%; Score 42.2; DB 10; Length
Best Local Similarity 51.2%; Pred. No. 0.065;
Matches 148; Conservative 0; Mismatches 138; Indels
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-26
PRIOR PRICH APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-27
PRIOR PRICH FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-20
                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NOS: 49117
                          Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 18355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nongbing
APPLICANT: Tao, Nongbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     981 TGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCAC 1040
                                                                                                                                                                                                                                                                                                                            921 AACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAGACGGAAGCATGGC 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 AACAGGAAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATTCTCCTAAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 TICAAGAIGGGAAIGCCICAGGGIAGCIAGCAIGGAAAAACAAAGCAAITIACAIAGAGI 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.41
INFORMATION: EST_HUMAN HIT: BE781438.1, EVALUE 1.60e+00
INFORMATION: SWISSPROT HIT: P11532, EVALUE 1.00e-17
INFORMATION: NT HIT: X06178.1, EVALUE 9.00e-63
                                                                                                                                                                                                             Length 122;
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48.6%; Pred. No. 0.039;
tive 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                      0; Indels
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CTHER INFORMATION: Clone ID: 46-LIB3058-032-Q1-K1-D10
US-09-960-352-10742
                                                                                                                                                                                                   6.0%; Score 122; DB 10;
100.0%; Pred. No. 1.5e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10742, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
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Sequence 18355, Application US/09864761
                                                                                                                                                                                                                                                        Matches 122; Conservative
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Matches 118; Conservative
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SEQ ID NO 10742 LENGTH: 436

TYPE: DNA

Query Match

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 204
                                                                              APPLICANT:
APPLICANT:
                                                                                                                        APPLICANT:
                                                                                                                                                 APPLICANT:
                                   APPLICANT:
                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 ATGGGAATGCCTCAGGGTAGCTAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAAT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 GGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAAACAGAAGAAAG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 AACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGT 519
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335 TCAAGATGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTT 394
                                                                                GAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGC 514
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2.0%; Score 40.6; DB 10; Length 425;
Best Local Similarity 46.3%; Pred. No. 0.19;
Matches 133; Conservative 0; Mismatches 154; Indels 0
                                                                                                                                                                                                                                                                                                  515 CAAGTACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAG 563
                                                                                                                                                                                                                                                                                                                           520 ACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: BOS taurus
CHER INCREMATION: Clone ID: 18-BOVMS1-007-Q1-E1-E5
US-09-960-352-4010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4010
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4010, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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; Sequence 204, Application US/09864864; Patent No. US20020102679A1

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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.

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APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C. APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nengappan APPLICANT: Mathialagan, Nengappan APPLICANT: Mathialagan, Negappan TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 16511.006/37-21(10298)C CURRENT APPLICATION UNMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.0%; Score 39.8; DB 10; Length 418; Best Local Similarity 47.1%; Pred. No. 0.32; Matches 122; Conservative 0; Mismatches 137: Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 428;
                                                                                                                                                                                              APPLICANT: Carter, Darrick TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 53-LIB3058-009-Q1-K1-F2
US-09-960-352-12395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 GGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0%; Score 40.4; DB 10;
53.1%; Pred. No. 0.22;
tive 0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                  Corixa Invention Disclosure Database
                                                                                                                                                                                                                                                         FILE REFERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12395, Application US/09960352 Patent No. US20020137139A1
Harlocker, Susan L.
                                                                        Lodes, Michael J.
                    Dillon, Davin C.
Secrist, Heather
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                                                                                                                                                                       Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.08
Best Local Similarity 53.18
Matches 86; Conservative
                                                                                               Algate, Paul A.
Fling, Steve P.
                                                                                                                                                  Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Homo sapiens
US-09-864-864-204
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400 GGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAG 459
                                     460 AACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGT 519
                                                                                                        369 AAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCCAGAATCAGAAACTGAAAGAGT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RESNICK, RICHER J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Guraham, James R.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNICLEOTIDES ENCODING NOVEL SECRETED PROTEINS
TITLE OF INVENTION: WUMBER: US/09/822,846
CURRENT APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Indels
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60.0%; Pred. No. 0.82;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                   ; Sequence 343, Application US/09822846
; Publication No. US20030027139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 183, Application US/10174590
Publication No. US20030008352A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steininger II, Robert J. Bowman, Michael R. Spaulding, Vikki Wong, Gordon G.
                                                                                                                                                                                                                                                                                                                                                                                McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merberg, David
Treacy, Maurice
Agostino, Michael J.
                                                                                                                                                           520 ACAACAACATAAGGTGCTT 538
                                                                                                                                                                                                173 ATCTAGACACAGAATCCTT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fechtel, Kim
Howes, Steven H
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.0%
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hilary
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Goddard, Audrey
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JS-09-822-846-343
                                                                                                                                                                                                                                                                                                                      ; Publication No. US20 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                           RESULT 12
US-09-822-846-343/C
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LENGTH: 1381
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APPLICANT:
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                                                                                                                  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMENBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343-816.42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT PILING DATE: 2002-06-18
PLIOR application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1281 AAAAACAATTTAAAATTTCAAATTTTAAAATTGCTCCACCATAAGATGAATAAAGAGC 1222
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60.0%; Pred. No. 0.91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 TGAATGACTGGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAA 478
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CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 183, Application US/10176758 Publication No. US20030008353A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 60.08;
                                                                             Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith, Victoria
Watanabe, Colin K.
Godowski, Paul J. Gurney, Austin L.
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Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.9%
Best Local Similarity 60.0%
Matches 66; Conservative
                                                          Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapien
US-10-174-590-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORGANISM: Homo Sapien US-10-176-758-183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                    SEQ ID NO 183
LENGTH: 1594
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                                                          APPLICANT:
APPLICANT:
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APPLICANT:
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RESULT 15

RESULT 15

Sequence 183, Application US/10175737

Sequence 183, Application US/10175737

Publication No. US2003001315341

Sequence 183, Application No. US20030013153A1

Sepulcant: Baker, Kevin P.

APPLICANT: Baker, Kevin P.

APPLICANT: Goddard, Audrey, Austin L.

APPLICANT: Goddard, Audrey, Austin L.

APPLICANT: Godray, Austin L.

APPLICANT: Godray, Austin L.

APPLICANT: Watanabe, Colin K.

APPLICANT: Abang, Mannaber, Colin K.

APPLICANT: Watanabe, Colin K.

APPLICANT: Abang, Mannaber, Colin K.

APPLICANT: Application removed - See File Wrapper or Palm

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Search completed: April 25, 2003, 23:58:03 Job time: 140.776 secs

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Query Match
1.9%; Score 39.6; DB 9; Length 1594;
Best Local Similarity 60.0%; Pred. No. 0.91;
Matches 66; Conservative 0; Mismatches 44; Indels 0;

Title:

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16150.348 Million cell updates/sec
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/SIDSZ/gogdata/geneseq/geneseqn-embl/Na1982.DAT:*
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/SIDSZ/gogdata/geneseq/geneseqn-embl/Na1984.DAT:*
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2185239 seqs, 1125999159 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 5000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Transfer Breeze Comment	Adaman dystrophin m	Adeno-associated v	Adeno-associated v	Human dystrophin m	Adeno-associated v	Adeno-associated v	Human dystrophin m	Human dystrophin r	Human dystrophin m
SUMMARIES	ID		AAD37234	AAD37256	AAD37262	AAD37237	AAD37357	AAD37363	AAD37220	AAD37232	2007/2000 AMD37330	AAD3/238
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ALIGNMENTS

RESULT 1

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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                  New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain,
                                                                            Human dystrophin minigene delta3990.
        AAD37234 standard; DNA; 3999 BP.
                                                                                                                                                                                                                    27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                          28-APR-2000; 2000US-200777P.
                                                      21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                             WPI; 2002-049342/06.
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                                                                                                                                                                                                                                                                (XIAO/) XIAO X.
                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                             08-NOV-2001.
                               AAD37234;
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AAD37234
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rod repeats, H1 and H4 domains and a cysteine rich domain of Example 1; Page 46-47; 71pp; English. dystrophin gene

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin game, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domains and cysteine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3990 containing nucleotides 1-1668 (N-terminus, dystrophin minigene delta3990 containing nucleotides 1-1668 (N-terminus, hinge H1 and rods R1 and R2), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

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Sequence 3999 BP; 1223 A; 907 C; 933 G; 936 T; 0 other;

Gaps DB 24; Length 3999; ; 0 Indels ; 0 0; Mismatches 100.0%; Score 2041; 100.0%; Pred. No. 0; Best Local Similarity 100.0 Matches 2041; Conservative Query Match

1 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 60

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181 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 240

241 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 300

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1380 GAAAGAGTIGAATGACTGGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAGA 1439

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TGATGAATCTAGTGGAGATCACGCAACTGCTTTTGGAAGAACAACTTAAGGTATTGGG 600

AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACGCTGGGTTCTTTTACAAGACCA 1679 AGAICGAIGGGCAAACAICIGIAGAIGGACAGAAGACCGCIGGGIICITITACAAGACCA 660 1560 TGATGAATCTAGTGGAGATCACGCAACTGCTGTTTGGAAGAACAACTTAAGGTATTGGG 601

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1741 CCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCT 1800 1801 GAACACCAGAIGGAAGCIICIGCAGGIGGCCGICGAGGACCGAGICAGGCAGCIGCAIGA 1860 1621 GCAGCCCGTGGGCGATCTCCTCTTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGC 1680 1681 ACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCG 1740 2700 ACTICGAGGAGAAATIGCGCCTCTGAAAGAGAACGIGAGCCACGICAAIGACCTIGCTCG 2759 2460 CACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 2519 1501 GCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCA 1560 2699 1441 CACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 1500 1321 TGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGG 1380 2159 1021 AAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGA 1080 1201 GCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGC 1260 1261 AGTICAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACC 1320 1920 TAAGGAAAGCCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGA 1979 961 CCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCA 1020 781 CITGAIGITGGAGGTACCTACTCATAGAITACTGCAACAGTTCCCCCTGGACCTGGAAAA 840 721 GGTGACACCAGCTGGGTTACTAAGGAAACTGCCATCTCCAAACTAGAAATGCCATCTTC 780 2760 CCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCT 901 TAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAAGAGCTGATGAAACAATGGCAAGA 1081 TAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCCATTT 841 GITTCTTGCCTGCCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCCG g QΥ ò q QΥ a ŏλ q pp δλ g g δ δλ g ŏ δ qq δy g qq QQ δŏ a δλ ò g Qγ

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28'20 GAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGA 2879
                       1921 CTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAAC 1980
                                                              AAD37256 standard; DNA; 4966 BP
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.

Adeno-associated virus vector plasmid, AAV-MCK-delta3990.

(first entry)

21-AUG-2002

Chimeric - Homo sapiens Chimeric - Unidentified

WO200183695-A2

27-APR-2001; 2001WO-US13677

28-APR-2000; 2000US-200777P

(XIAO/) XIAO X.

Xiao X;

WPI; 2002-049342/06

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene

Example 1; Page 59-60; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.

Sequence 4966 BP; 1403 A; 1216 C; 1232 G; 1115 T; 0 other;

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                                                                                                                                                                                                                                                                                                                    TGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 120
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                                              1 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC
                                                                                                                                                  121 CCAGTITCATACTCATGAGGGGTACATGGATTTGACAGGCCCATCAGGGCCGGGTTGG
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                                                                                                                                                                                                                                                    241 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC
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100.0%; Score 2041; 100.0%; Pred. No. 0;
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AAD37262

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CIGGGAGAGACCATCTCGCCAAACAAGTGCCCTACTATATCAACCACGAGACTCAAAC 1980
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                               1081 TAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAGTCTCTCAACATTAGGTCCCATTT 1140
                                          3397 GCAGCCCGTGGGCGATCTCCTTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGC
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression scottrol element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -
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                                                                                                                                       Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
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                                                                                                    Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3990.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches
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AAD37262 standard; DNA; 4990 BP.
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                                                                                                                                                                                                                   Chimeric - Homo sapiens.
Chimeric - Cytomegalovirus.
Chimeric - Unidentified.
                                                                         21-AUG-2002 (first entry)
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1 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAG	GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACAACATGGAGTG 1111111111111111111111111111111	1 AGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTCACTCA	1 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG	1 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACCA 		GGTGACACAACCTGTGGTTACTAAGGAAACTGCCATCTCCAAACTAGAAATGC 	CTTGATGTTGGAGGTACCTACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAA 	GTTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCCCC	TAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGA 				GGAAGCCAGTICTGACCAGTGGAAGCGTCTGCACTTTCTCTGCAGAACTTCTGGTGTG 1	· · · · - ·	ATGTACATAGGCCTTCAAGAGGGAATTGAAAACTAAAGAACC ATGTACATAGGCCTTCAAGAGGGAATTGAAAACTAAAGAACC ATGTACAAAAGAGCCTTTAAAAAAAAAA	TGTAATCATGAGTACTTTGAGACTGTAGGAATATTTCTGACAGAGCAGCCTTTGGAAGG 1
241 2041 . 301 . 2101 361 2161	0 0	48]	541	601	661	721	781	841	901	961 2761	1021 2821	1081 2881	1141	1201	1261	1321
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1381 ACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGT 1440
                                          1181 ACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGGCCCAGAATGT 3240
                                                                                                                  1501 GCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCA 1560
                                                                                                                              Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
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                                                                                                                                                                       GCAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGC 1680
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                                                                                   3241 CACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT
                                                                                                                                                          1561 AGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTG
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28-APR-2000; 2000US-200777P. (XIAO/) XIAO X. ××

WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -

Example 1; Page 48-49; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domarins and cysteine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3849 containing nucleotides 1-1668 (N-terminus, hinge H1 and rods R1, R2), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

Sequence 3858 BP; 1189 A; 866 C; 905 G; 898 T; 0 other;

Indels 141; Gaps vuery Match 85.7%; Score 1749; DB 24; Length 3858; Best Local Similarity 93.1%; Pred. No. 0; Mismatches 1900; Conservative 0; Mismatches

1020 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 1079 1 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 60 ò g

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541 TGATGAATCTAGTGGAGATCACGCAACTGCTGTTTGGAAGAACAACTTAAGGTATTGGG 600

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1561 AGAGGCCACGGATGAGCTGGACCTCAAGCTGCCCAAGCTGAGGTGATCAAGGGATCCTG 1620 2439 AGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGGATCATCAGGGATCTG 2498 1621 GCAGCCCGTGGGGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGC 1680 1381 ACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGT 1440 2259 ACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGGCCCAGAATGT 2318 1441 CACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 1500 2319 CACTCGGCTTCTACGAAACCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 2378 1501 GCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCA 1560 1321 TGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGG 1380 1899 AAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGA 1958 1081 TAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAGTCTCTCAACATTAGGTCCCATTT 1140 1141 GGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGT 1200 1201 GCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGC 1260 2079 GCIACAGCIGAAAGATGATTAAGCCGGCAGCACCTATTGGAGGCGACTTTCCAGC 2138 1261 AGTTCAGAACCAGAACGATGTACATAGGCCTTCAAGAGGGAATTGAAAACTAAAGAACC 1320 ---- 1677 1560 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG 1619 1620 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACGCTGGGTTCTTTACAAGAC-- 1677 781 CITGAIGITGGAGGTACCTACTCATAGATACTGCAACAGITCCCCCTGGACCTGGAAAA 840 841 GTTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCG 900 901 TAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGA 960 661 GCCTGACCTAGCTCCTGGACTGACCACTATTGGAGCCTCTCCTACTCAGACTGTTACTCT 720 721 GGTGACACCAACCTGTGGTTACTAAGGAAACTGCCATCTCCAAACTAGAAATGCCATCTTC 780 601 AGAICGAIGGGCAAACAICIGIAGAIGGACAGAAGACGGCIGGGIICTITIACAAGACCA 660 2139 AGTICAGAAGCAGAACGAIGTACAIAGGGCCTICAAGAGGGAATIGAAAACIAAAGAACC 1021 AAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGA 961 CCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCA 1959 TAACATGAACTICAAGTGGAGTGAACTICGGAAAAAGTCTCTCAACATTAGGTCCCATTT 1678 -----1678 ---ρģ δλ g Db δ g qq δλ g Qγ ò qq pp δy g QΩ g ΩŊ . Dp δλ δy qq δ ò δ g δy qq δy δλ q Qγ

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2499 GCAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGC 2558
                                                                             1741 CCAGCTTACCACTTTGGGCATTCAGCTCTCACGTATAACCTCAGCACTCTGGAAGACCT 1800
                                                                                                                                1801 GAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGA 1860
                                                                                                                                               2679 GAACACCAGATGGAAACCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGA 2738
                                                                                                                                                                                    1861 AGCCCACAGGGACTITGGTCCAGCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCC 1920
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RESULT 5 AAD37257

AAD37257 standard; DNA; 4825 BP. AAD37257;

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21-AUG-2002 (first entry)

Adeno-associated virus vector plasmid, AAV-MCK-delta3849.

Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.

Chimeric - Homo sapiens. Chimeric - Unidentified.

WO200183695-A2.

08-NOV-2001

27-APR-2001; 2001WO-US13677.

28-APR-2000; 2000US-200777P.

(XIAO/) XIAO X.

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WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, HI and H4 domains and a cysteine rich domain of a dystrophin gene.

Example 1; Page 61-62; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The

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invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                            2197 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACAACAAGAGGTGCTTCA 2256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 120
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                                                                                                                                              Sequence 4825 BP; 1369 A; 1175 C; 1204 G; 1077 T; 0 other;
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                                                                                                                                                                                                                                                                                   IGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGG 1380
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                                                                                                                                                                                      1141 GGAAGCCAGTICTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTG 1200
                                                                         1021 AAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGA 1080
                                961 CCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCA 1020
2476 GTTTCTTGCCTGGCTTACAGAAGCTGAAACAGCTGCCAATGTCCTACAGGATGCTACCG 2535
                     901 TAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGA 960
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cystelne-rich domains of dystrophin or utrophin genes. The domprishing dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV dystrophy (BMD) in a mammalian subject. The present sequence is AAV cector plasmid construct containing human dystrophy minigenes, a cytomegalovirus (CMV) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                   Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BECKer muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1800 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 1859
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1 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 60
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                                                                                                                                                                                                                                                                                                   Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4848 BP; 1405 A; 1144 C; 1180 G; 1119 T; 0 other;
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                                                                                                                                                                                                    AAD37263 standard; DNA; 4848 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                                      - Cytomegalovirus.
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Matches 1900; Conserv
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186	192	19	24	301	36	42.	48.	541	601 2400	99	2458	2 2	781	4 4	2499	901	961 2619	1021	1081 2739	1141
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1201 GCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGC 1260
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2799 GGAAGCCAGTICTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTG 2858
                                                                                                                                                                                                                                                                        2919 AGTICAGAAGGAGAAGGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACC 2978
                                                                                                                                                                                                                                                                                                                                                                                TGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGG 1380
                                                                                                                                                                                                                                                                                                                                                                                                                        1381 ACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCCAGAATGT 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1441 CACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1501 GCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCA 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1561 AGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTG 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1621 GCAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGC 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1681 ACTICGAGGAGAAATIGCGCCTCTGAAAGAGAACGTGAGCCACGICAATGACCTIGCICG 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1741 CCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCT 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1921 CTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAAC 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1981 AACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAA 2040
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
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Homo sapiens.

WO200183695-A2.

08-NOV-2001

27-APR-2001; 2001WO-US13677.

28-APR-2000; 2000US-200777P

(XIAO/) XIAO X.

WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a

Example 1; Page 43-44; 71pp; English.

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta4173 containing nucleotides 1-1992 (N-terminus, hinge H1 and rods R1, R2 and R3), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

Sequence 4182 BP; 1309 A; 927 C; 970 G; 976 T; 0 other;

Pred. No. 0; 0; Mismatches 72; Indels 183; Gaps 83.4%; Score 1702.8; DB 24; Length 4182; 88.5%; Pred. No. 0; Matches 1969; Conservative Best Local Similarity Query Match

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- 1080 recreaggacacarrecaagcacaaggagagarreraargargreggaagregaaaga 1139 61 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 120 οy
- 121 CCAGITICATACICAIGAGGGIACAIGAIGGAITIGACAGCCCCAICAGGGCCGGGIIGG 180
- 181 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 240 ò
- 241 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 300 g

g

- 301 TAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAAACT 360
- 1320 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 1379

2400 GIGGCIACAGGIGAAAGAIGAAITAAGCCGGCAGGCACCIATIGGAGGCGACITICC 2459 1258 AGCAGTICAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGA 1317 2460 AGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGAATTGAAAACTAAAGA 2519 1138 TTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGT 1197 1018 CCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTT 1077 1860 GGGCAAACTGTATTCACTCAAACAAGATCTTTCAACACTGAAGAATAAGTCAGTGAC 1919 1920 CCAGAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAA 1979 1980 ACTIGAAAAGAGTACAGCACAGACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGA 2039 958 AGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAAAG 1017 1680 CCITCICAAAIGGCAACGTCITACIGAAGAACAGIGCCIITTIAGIGCAIGGCTIICAGA 1739 1740 AAAAGAAGATGCAGTGAACAAGATTCACACAGCTGGCTTTAAAGATCAAAATGAAATGTT 1799 1380 GAAAGAGTIGAATGACIGGCTAACAAAAACAGAAGAAAAAAGAAAAAGAAAAATGGAGGAAGA 1439 601 AGATCCATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACCA 660 661 GCCTGAC-----CTAGCTCCTGGACTGACCACTATTGGAGCCTCTCCTACTCA 708 709 GACTGTTACTCTGGTGACACA-----ACCTGTGGTTACTAAGGAAACTGCCATCTC 759 541 IGAIGAATCIAGIGGAGAICACGCAACIGCIGCTITGGAAGAACAACIIAAGGIAIIGGG 600 421 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 480 838 AAAGTITCIIGCCIGGCTTACAGAAGCIGAAACAACTGCCAATGICCIACAGGAIGCIAC 760 -------CAAACTAGAAATGCCATCTTCCTTGATGTTGGAG-----_____ 092 794 ----ΩD ŏλ g g δλ ΩD Dp Óγ qq Öλ g Óγ qq

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1318 ACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGA 1377
                                                   1438 TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAA 1497
                                                                                                                                                                 CCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACT 1557
                                                                                                                                                                              1558 TCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATC 1617
                                                                                                                                                                                                                                    GGCACTICGAGGAGAAAITGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGC 1737
                                                                                                                                                                                                                                                                                                                                                2880 GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGC 2939
                                                                                                                                                                                                                                                                                                                                                                                       TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGGACTCTGGAAGA 1797
                                                                                                                                                                                                                                                                                                                                                                                                       Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1918 TCCCTGGGAGAGGCCATCTCGCCAAACAAGTGCCCTACTATATCAACCACGAGACTCA 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1978 AACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAA 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human dystrophin rod, hinge and CR domain regions encoding DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD37232 standard; DNA; 2169 BP.
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 invention and cysteine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control control element. The dystrophin minigene in operable linkage with an expression useful for treating Duchenne mascular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human of the dystrophy in DNA fragment encoding rods R22, R23 and R24, hinge H4 and
                                                                                                                                                           New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           980 GCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCTG 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1040 GAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGG 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1100 AGTGAACTICGGAAAAAGTCTCTCAACATTAGGICCCATTIGGAAGCCAGTTCTGACCAG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1160 TGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGGTGAAAGATGAT 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              800 ACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACA 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2169 BP; 623 A; 529 C; 524 G; 493 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.9%; Score 1242; DF 100.0%; Pred. No. 0; tive 0; Mismatches
                                                                                                                                                                                                                                    Example 1; Page 45-46; 71pp; English.
               27-APR-2001; 2001WO-US13677.
                                           28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1242; Conservative
                                                                                                                                  WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                        dystrophin gene
                                                                        (XIAO/) XIAO X.
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
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                                                                                                                                                                                                                                                                                                                                                                                             1820 CIGCAGGIGGCCGICGAGGACCGAGICAGGCAGCIGCAIGAAGCCCACAGGGACITIGGI 1879
                                                                                                                                                                                                                                                                                                                                                                                                        1760 ATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTT 1819
                                                                                                                                                                                                                                                                                                                                                           1580 GACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTC 1639
                                                                                                                                                                                                                                              1640 CICATIGACICICCCAAGAICACCICGAGAAAGICAAGGCACTICGAGGAGAAAIIGCG 1699
                                                                                                                                                                                                                                                                                             1700 CCTCTGAAAGAAAGGTGAGGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGC 1759
                                                                                                                                              1520 AGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTG 1579
1340 GAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAACTCTACCAG 1399
                                               1400 GAGCCCAGAGAGCTGCCTCCTGAGGAGAGGCCCAGAATGTCACTCGGCTTCTACGAAAG 1459
                                                                                                                                                                                                            602 GAGCCCAGAGAGCTGCCTCCTGAGGAGAGCCCCAGAATGTCACTCGGCTTCTACGAAAG
                                                                                                1460 CAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000 AAAATGACAGGCTCTACCAGTCTTTAGCTGACCTGAATAAT 2041
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domerior and cysteine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is control element, in a mammalian dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3531 containing nucleotides 1-1341 (N-terminus, hinge HI and rod RI), 8059-10227 (rods R22, R23 and R44, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1891 GAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAG 1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1340 GAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAG 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGAT 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1220 GAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGAT 1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1831 GIACATAGGGCCTICAAGAGGGAATIGAAAACTAAAGAACCTGTAATCAIGAGTACTCTT 1890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     920 GACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     860 GAAGCIGAAACAACIGCCAAIGICCIACAGGAIGCIACCGGIAAGGAAAGGCICCIAGAA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 800 ACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.9%; Score 1242; DB 24; Length 3531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3531 BP; 1071 A; 809 C; 824 G; 827 T; 0 other;
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0
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tive 0; Mismatches
                                                                                                                                                                              Example 1; Page 50-51; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 1242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                               WPI; 2002-049342/06.
(XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                  Xiao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1160
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a

WPI; 2002-049342/06.

Example 1; Page 62-63; 71pp; English.

dystrophin gene -

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1460 CAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAG 1519
1400 GAGCCCAGAGAGCTGCCTCCTGAGGAGAGGCCCAGAATGTCACTCGGCTTCTACGAAAG 1459
                                                                    2011 CAGGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAACCTGCACTCCGCTGACTGGCAG 2070
                                                                                                       1520 AGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTG 1579
                                                                                                                   1580 GACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTC 1639
                                                                                                                                                                        CTCATTGACTCTCTCCAAGATCACCTCGAGAAGTCAAGGCACTTCGAGGAGAAATTGCG 1699
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                                                                                                                                                                                                                                                                                                                 1760 ATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTT 1819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000 AAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 2041
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spectrin;
                                                                                                                                                                                                        Human; dystrophin minigene; muscular; gene therapy; utrophin; sadeno-associated virus; AAV; Duchenne muscular dystrophy; DMD;
                                                                                                                                                                 Adeno-associated virus vector plasmid, AAV-MCK-3531.
                                     AAD37258 standard; DNA; 4498 BP.
                                                                                                                                                                                                                                                  Becker muscular dystrophy; ds.
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                            Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                        WO200183695-A2
                                                                                                                         21-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2001.
                                                                                 AAD37258;
RESULT 10
                      AAD37258
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X × 27-APR-2001; 2001WO-US13677 28-APR-2000; 2000US-200777P

(XIAO/) XIAO X.

Xiao X;

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      980 GCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCTG 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1040 GAAGGTTCCGATGATGCAGTCCTGTTACAAGACGTTTGGATAACATGAACTTCAAGTGG 1099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        860 GAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGGTAAGGAAAGGCTCCTAGAA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      920 GACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAA 979
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 4498 BP; 1251 A; 1118 C; 1123 G; 1006 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           60.9%; Score 1242; Di
100.0%; Pred. No. 0;
tive 0; Mismatches
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Matches 1242; Conservative
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain,
                                                                                                                                                                                                                                                                                                      1820 CTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGT 1879
                                                                                                                                                                                                                                                                                                                                                      1880 CCAGCATCTCAGCACTTTCTTTCCACGTCTGTGCAGGGTCCCTGGGAGAGAGCCATCTCG 1939
                                                                                                                                                                                                                                                                                                                                                                               3188 ccascarcricascarrircrirccacgrerecassescreegesassasceareres 3247
                                                                                                                                                                                                                                                                                                                                                                                                        1940 CCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAAACAACTTGCTGGGACCATCCC 1999
                                                                                                                                                                                                                                                                                                                                                                                                                      1760 ATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTT 1819
                                                                                                                                                   1640 CICATIGACICICICCAAGAICACCICGAGAAAGICAAGGCACTICGAGGAGAAAIIGCG 1699
                                                                                                                                                                 1700 CCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGC 1759
                                                                                                                                                                                                                 3008 CCICTGAAAGAGAAAGTGAGCCACGCCAATGACCTTGCTCGCCAGCTTACCACTTTGGGC 3067
                                                                                                                                                                                                                                                                           ATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTT 3127
                                                1520 AGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGGTG 1579
                                                               2768 CAGGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAACCTGCACTCGCTGACTGGCAG 2827
1460 CAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAG
                                                                                                                                                                                                                                                                                                                                                                       Human dystrophin minigene delta3510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD37240 standard; DNA; 3510 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200183695-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-2001.
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                                                                                                                                                                                                                                                                                      3068
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression clement. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular useful for treating manners.
                                                                                                                                                                                                                                     dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3510 containing nucleotides 1-1668 (N-terminus, hinge H1 and rods R1 and R2), 8407-10227 (rods R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTACAAGACCA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 GCCIGACCTAGCTCCTGGACTGACCACTATTGGAGCCTCTCCTACTCAGACTGTTACTCT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 TGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1080 IGCTGAGGACACATTGCAAGGACACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 GCCICITGGACCTGAICTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 480
                                                                                                                                                                                                                                                                                                                                                                                                                            181 TAATATICIACAATIGGGAAGTAAGCIGATIGGAACAGGAAAATIATCAGAAGAIGAAGA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TGCTGAGGACACATTGCAAGGACACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                             Indels 489; Gaps
                                                                                                                                                                                                                                                                                                                                                           Ouery Match 51.6%; Score 1053; DB 24; Length 3510; Best Local Similarity 76.0%; Pred. No. 1.3e-288; Matches 1552; Conservative 0; Mismatches 0; Indels 489;
rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                            Sequence 3510 BP; 1073 A; 787 C; 828 G; 822 T; 0 other;
                                                      Example 1; Page 51-52; 71pp; English.
                              dystrophin gene -
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Db 2331 GAACACCAGATGGAGGTGGCCGTCGAGGACCAGATCGATGA 2390 Qy 1861 AGCCCACAGGACTTTGGTCCAGCATCTACTTTCCAGGTCTGTCCAGGTC 1920 1861 AGCCCACAGGGACTTTGGTCCAGCATTTCTTTCCAGGTCTGTCCAGGTC 1920 1861 AGCCCACAGGGACTTTGGTCCAGCATTTCTTTCCAGGTCTTGTCCAGGGTC 2450 1921 CTGGGAGAGGCCATTTGGTCCAGCATTCTTTCTTTCCAGTCTGTCCAGGGTC 2450 1921 CTGGGAGAGGCCATCTCGCCAACAAGTGCCCTACTATTCTACCAGGTCC 2450 111111111111111111111111111111111111	RESULT 12 AAD37259 ID AAD37259 standard; DNA; 4476 BP. XX XX XX AD37259; XX DT 21-AUG-2002 (first entry) XX M Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; XX XX XX M Human; dystrophy ds. XX	New d dystr dystr dystr dystr. Examp Examp The pa dysis a dysis a dysis invent comprise controller dystro vector creatings
QY 721 GGTGACACCTGTGGTTACTAAGGAAACTGCCATCTCCAAACTAGAATGCCATCTTC 780 Db 1677	2y 108 2y 108 3b 167 3y 1143 3b 1673 3y 1203 4y 1261 5b 1731 6b 1731 7y 1261 7y 1261 7y 1261 7y 1381 7y 1381 7y 1381 7y 1381 7y 1381 7y 1381 7y 1381	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

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2331 GAACACCAGAIGGAAGCTICIGCAGGIGGCCGTCGAGGACCGAGGTCAGGCACCAGATGGAAGCTICIGCAGGCGCGTCGAGGACCAGCAGCAGCAGGAAGCAGA
                                                               1861 AGCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTTCCACGTCTGTCCAGGGTCC 1920
                                                                                      2451 CTGGGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAAC 2510
                                                                                                                                               1921 CTGGGAGAGACCATCTCGCCAAACAAAGTGCCCTACTATGAACCACGAGAGTCAAAC 1980
                                                                                                                                                                                                                                                        1981 AACTIGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAA 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lew dystrophin minigene for treating Duchenne or Becker muscular lystrophy comprises an N-terminal domain or modified N-terminal domain, od repeats, H1 and H4 domains and a cysteine rich domain of a lystrophin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adeno-associated virus vector plasmid, AAV-MCK-3510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xample 1; Page 63-65; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD37259 standard; DNA; 4476 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-2001; 2001WO-US13677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Homo sapiens.
Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                                                                   2041 T 2041
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Match 51.6%; Score 1053; DB 24; Length 4476; Cocal Similarity 76.0%; Pred. No. 1.5e-28%; Indels 489; Gap. ss 1552; Conservative 0; Mismatches 0; Indels 489.	CTTTC 60	61 TGCTGAGGACACATTGCAAGCACAAGGAGAGTTTCTAATGATGTGGAGTGGTGAAAGA 120 	121		241	301 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 360 301 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 2135	2016 TAGCATGGAAAAACAAAGCAATITACATASAATTATATATATATATATATATATATATATATA	480			541	5310 TGATGAALCIAGIOMONIO CONTROL CONTROL CONTROL CANDROL CANDROL CONTROL CANDROL CANDR	720	1 GCCTGACCTAGCTCTGGACTGACTGTTTGGAGCCTCTCCTACTCAGACTGTTACTCT 7-2	2433	- 2	2433	781 CTTGATGTTGGAGGIACCI	2433	841 GTTT	2433	901 TAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAAAGGCTOALGAAGGTCTCTAGAAGTCTCTAGAAGGGAGTAAAAAGAAGTTAAAAGGGAGTAAAAAGAAG	2433	961 CCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGAALGAAAACACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	2433	1021 AAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACCAATGCTTCCTGTTACCAATGCTTCCTGTTACAATGCTTCCTGTTACAATGCTTCCTGTTACAATGCTTCTTCTTTACAATGCTTCCTGTTACAATGCTTCTTTTACAATGCTTCTTTTACAATGCTTCTTTTACAATGCTTCTTTTACAATGCTTCTTTTACAATGCTTCTTTTACAATGCTTCTTTTTACAATGCTTCTTTTTTTT
Query Best Match	γ d	· > 5	:	a & 4	a Ko	g &	Oy Oy	q à	g 2	ò	δλ	go Ao	QQ	Qy	Ω	Qy	Dρ	οy	qq	ΟŊ	qq	οy	QQ	ΟŊ	qq	č

Oy Db Oy Db

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13 1 13 13	YAN!	ACCTTTCTCTGCA(CAGGCACCTATTGGAGGCGACTTTCCAGC 126(TTCAAGAGGAATTGAAAACTAAAGAACC 1320 	ATA - ATA	TECCT CTGCCT	150(278	TGAGACCCTTGAAAGACTCCAGGAACTTCA 1560 	GCCAL	rctccaagatc 	GTGAGCCACGTC	GTGAGCCCACGCCACTCGCAGAGACCT 180 TATAACCTCAGCACTCTGGAAGACCT 180	CACCGTATAACCTCAGCACTCTGGAAGACCT	CCTCGAGGACCAAGTCAGCAGCTGCATCA 314	AGCACTTTC	TGCCCTACTATATCAACCACGAGACTCAAAC 191		TCTACCAGTCTTTAGCTCACCTGAGTAA 20. 		
	ACATGAACTTCAAGTGGAGTGAACTTCG	GGAAGCCAGTTCTGACCAGTGGAAGCGTCT	GCTACAGCTGAAAGTGATGAATTAAGCCG GCTACAGCTGAAAGTGATGAATTAAGCCG	GCIACACAGGGGGAAGGATGTACATAGGGC AGTTCAGAAGCAGAAGATGTACATAGGGC	7 AGTICAGAAGCANAACCIITGAGACTGTACC 1 TGTAATCATGAGACTGTACC	TGTAATCATGAS ACTOT CONTROL OF TARGET CONGAGA TA ACTOT ACCAGGAGCCCAGAGA THIN THIN THIN THIN THIN TA ACTOT ACCAGGAGCCAGAGAG	1 CACTCGGCTTCTACGAAAGCAGGCTGAGG 1 L1111111111111111111111111111111111	1 GCACTCCGCTGACTGGCAGAGAAAAT	7 GCACTCCCCIGACIAGOSCICICATA 1 AGAGGCCACGGATGAGCTGGACCTCAA 1 1111111111111111111111111111111111	47 AGAGGCCACGGATGAGTTGCTCTCATTGACT	07 GCAGCCCGTGGGCCATCTCCTCATA 81 ACTTCGAGGAGAAATTGCGCCTCT	67 ACTTCGAGGAGAAATTGGGCCTC' 41 CCAGCTGACCACTTTGGGCATTG	27 CCAGCTTACCACTTTGGGCATTCAGCTC	01 GAACACCAGATGGAAGCTTCTGCAGGTG 	61 AGCCCACAGGGACTTTGGTCCAGCATCT	147 AGCCCACAGGGACTTTGGTCCAGCAICT 021 CTGGGAGAGGCCATCTCGCCAAACAAA	207 CTGGGAGAGAGCCATCTCGCC	981 AACTTGCTGGGACCATCCCAAAATG 	041 T 2041	327 T 332

RESULT 13

AAD37241

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241 GAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGTCACTCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A gene encoding a shortened dystrophin - useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ48568 standard; cDNA to mRNA; 4402 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dystrophin gene; truncated; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0142134.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY59239.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ48568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XX
                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control element, The dystrophin minigene operably linked to an expression control control element, in a recombinant adeno-associated virus or retrovirus is dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin DNA fragment encoding rods R23 and R24, hinge H4 and CR
                                                                                              Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                    New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1147 CAGITCIGACCAGIGGAAGCGICIGCACCITICICIGCAGGAACTICIGGIGGGTACA 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1207 GCTGAAAGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCA 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1267 GAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAAT 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1327 CATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1387 GAAACTCTACCAGGGGCCCAGAGGTGCCTCCTGAGGAGAGGCCCAGAATGTCACTCG 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human dystrophin rod, hinge and CR domain regions encoding DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24; Length 1821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1821 BP; 506 A; 451 C; 447 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%; Score 895; DB 24; L
100.0%; Pred. No. 8.1e-244;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 52-53; 71pp; English.
AAD37241 standard; DNA; 1821 BP.
                                                                                                                                                                                                                 27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                         28-APR-2000; 2000US-200777P.
                                               21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                              WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                   WO200183695-A2.
                                                                                                                                                                                                                                                                 (XIAO/) XIAO X.
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                          08-NOV-2001.
                        AAD37241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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1447 GCTICTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTC 1506
                                             1567 CACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCC 1626
               1627 CGTGGGCGATCTCCTCATTGACTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCG 1686
                                                                                                                                                                                    1687 AGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCT 1746
                                                                                                      1747 TACCACTITGGGCATTCAGGTCTCACGGTATAACCTCAGCACTCTGGAAGACCTGAACAC 1806
                                                                                                                                                                                                                                                                              1807 CAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCA 1866
                                                                                                                                                    1867 CAGGGACTTTGGTCCAGCATCTCAGCACTTTCCACGTCTGTCCAGGGTCCCTGGGA 1926
                                                                                                                                                                                                                                            1927 GAGAGCCATCTCGCCAAACAAAGTGCCCTACTATTAACAACAGGAGACTCAAACAACTTG 1986
                                                                                                                                                                                                                                                                                          A rod shortened dystrophin (deltaDysAH3) encoding nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     1987 CIGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscular dystrophy; rod domain; adeno-associated virus; AAV;
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                                 The invention provides a gene for the treatment of muscular dystrophy having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medalum consisting of an adeno-associated virus (ANV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low immune reaction. The present sequence represents a rod shortened
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 IGAIGAAICTAGIGGAGAICACGCAACIGCTGCTITGGAAGAACAACTIAAGGIAITGGG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1515 TAGGATGGAAAAACAAAGCATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACATAAGGTGCTTCA 480
                                                                                                                                                                                                                                                                                                                                                                                                                       301 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 360
                                                                                                                                                                                                                                          181 TARTATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AACTGAAGTACAAGAGGAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 300
                                                                                                                                                                                                                                                                                                                                                    121 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 180
                                                                                                                                                                                                                                                                                                61 TGCTGAGGACACATTGCAAGGACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 120
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                        DB 21; Length 4402;
                                                                                                                                                            Sequence 4402 BP; 1339 A; 984 C; 1010 G; 1069 T; 0 other;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                         32.3%; Score 658.4; DB 21;
97.7%; Pred. No. 2.8e-176;
tive 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1875 CCTTCTCAAATGGCAACGTCTTAC 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 GCCTGACCTAGCTCCTGGACTGAC 684
                    Claim 7; Page 21-22; 44pp; Japanese.
                                                                                                                                          dystrophin encoding sequence.
                                                                                                                                                                                                                           Matches 668; Conservative
                                                                                                                                                                                                               Local Similarity
muscular dystrophy
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
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AAD37260 standard; DNA; 4414 BP.

AAD37260;

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified to a spectrin gene, H1 and H4 N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cystrophin eriot domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control comprising dystrophin minigene operable linkage with an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAAATCAGAAACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1837 TGCTGAGGACACATTGCAAAGCACAAGGAGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AACTGAAGTACAAGAGGAGGAGTGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CCAGITICAIACTCAIGAGGGGTACAIGAIGGATITGACAGCCCAICAGGCCGGGTIGG 180
                                                                                                                                                                                                                                                                                                                                                                                              New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                    Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24; Length 4414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4414 BP; 1255 A; 1075 C; 1086 G; 998 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                            Adeno-associated virus vector plasmid, AAV-MCK-3447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.3%; Score 658.4; DB 24;
97.7%; Pred. No. 2.8e-176;
97.7%; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 65-66; 71pp; English.
                                                                                              Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                              27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                               28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 668; Conservative
       21-AUG-2002 (first entry)
                                                                                                                                     Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dystrophin gene -
                                                                                                                                                                                                                                                                                                                    (XIAO/) XIAO X.
                                                                                                                                                                                      WO200183695-A2.
                                                                                                                                                                                                                    08-NOV-2001.
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Search completed: April 25, 2003, 08:40:29 Job time : 361.763 secs

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17170.339 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                        OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 5000
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	Description	BI729851 603349511 BI730168 603349711 AL121550 DKRZp762L BM488464 PGHZD.PKO BC009242 HGMO Sapil BG212445 RST32032
SUMMARIES	ID	B1729851 B1730168 B1730168 BM488464 BC009242 BG212445
	DB	13 13 13 11 12
	Match Length DB ID	834 750 579 663 1490 784
æ :	Match	29.0 24.1 23.8 20.8 19.3
	Score	591.8 491.4 486.6 424.2 394.6 262.8
+[:::98	No.	H 22 W 4 W 70

source

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ALIGNMENTS

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B1/2/8031

834 bp mRNA linear EST 20-SEP-2001

803/49511F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5357162 5',
                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 834)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov e column: 03
High quality sequence stop: 796.
Location/Qualifiers
1. .834
                                                            шRNA
                                                         834 bp
                                                                                                                                                     BI729851.1 GI:15706864
                                                                                              mRNA sequence.
BI729851
                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                     house mouse.
                                                    BI729851
                                                                         DEFINITION
                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                           AUTHORS
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RESULT 1
BI729851
                                                                                                                                                   VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                     TITLE
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3;

3; Gaps

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/note="Organ: eye; Vetor: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTC-CGCT 1510
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                                                                                                                                                                                                                                                                                                                                                                                                            614 TACTCTGGAGACTGTGAGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACT
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                                                  /clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                      0; Mismatches
/organism="Mus musculus"
                /db_xref="taxon:10090"
/clone="IMAGE:5357162"
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603349711F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5357187 5',
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="reting"
/lab_host="reting"
/lab_host="reting"
/lab_host="reting"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MCC Library.

1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  958 AGACCICCAAGGIGAAA-TIGAAGCICACACAGAIGIITAICACAACCIGGAIGAAAACA 1016
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                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11908 row: f column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 GATGTTGGAGGTACCTACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAGTT 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 GCTGCTTGGGACAGAAACTCATAGATTACTGCAGCAGTTCCCTCTGGACCTGGAGAAGTT 128
                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procourement: The Cepto Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:5357187"
/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                 mRNA sequence.
BI730168
BI730168.1 GI:15707181
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88.48;
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                                                                                                                                              Mus musculus
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BM488464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 579) Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
1257 CAGCAGTTCAGAAGCA-GAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAA 1315
                                                                                                                            1316 GAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTTCTGACAGAGCAGCCTTTG 1375
                                                                                                                                                                                        1376 GAAGGACTAGAGAAACTCTACCAGGGGCCCAGAGAGCTGCCTCCTGAGGAGAGGCCCAG 1435
                 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                             957 AAGACCICCAAGGIGAAAIIGAAGCICACACAGAIGITIAICACAACCIGGAIGAAAAA 1016
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DKEZp762L078_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
DKEZp762L078 5', mRNA sequence.
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144 g 127 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.8%; Score 486.6; DB 9; Length 579; 97.2%; Pred. No. 4.1e-107; tive 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                           1436 AATGTCACTCGGCTTCTACGA 1456
                                                                                                                                                                                                                                                                          Contact: Ottenwaelder B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9
,11 weeks);growth plate(ld,7d,14d post-hatch)"
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
                                                                                                                                  1077 TGGATAACAFGAACTFCAAGFGGAGTGAACTFCGGAAAAAGTCFCTCAACAFFAGGFCCC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                     1137 ATTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGG 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGCACCTATTGGAGGCGACTTTC 1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cogburn, L.A. and Monsonego-Ornan, E. ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library, USDA/IFAFS Animal Genome
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University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-2822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1437 ATGTCACTCGGCTTCTACGAAAGCAGGCT 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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linear HTC 12-JUL-2001
/note="Vector: pcMySPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC009242

Homo sapiens, dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS270, DXS270, Clone IMAGE:3029414, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1480 TGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCT 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1420 TGAGGAGAGGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATAC 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1300 GGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCT 1359
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                                                                                                                                                                                                                                                                                                                                                                                                               1060 CCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAGTC 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 TGAGGAGAGGCCCCAGAATGTCACTAAAGTTCTCCGAAGGCAAGCAGATGATGATGTGTCAGNAC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000 CAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 CCTGTTGCAGAGACGTCTGGATAACATGAACTTCAGATGGAGTGAGCTTAGGAAGAAATC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                940 GCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTATCA 999
                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                             1 GCTCATGAAGCAGTGGCAGGATCTACAGGCAGAAATTGATGCACATACTGACATCT-TNN 59
                                                                                                                                                                       Query Match

20.8%; Score 424.2; DB 13; Length 663;
Best Local Similarity 78.1%; Pred. No. 5.6e-92;
Matches 518; Conservative 0; Mismatches 144; Indels 1;
                                                                                                                    6 others
                                                                                                                    144 t
                                                                                                                    172 g
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BC009242.1 GI:14714379
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                                                                                                                          SASE COUNT
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BC009242
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Homo sapiens

ORGANISM

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clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov series: IRAL Plate: 10 Row: j Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 503280 This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                                                                        contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1329 AACTGAAGTACAAGAGCAGATGAGTTCCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 1388
                                                                                                    Submitted (06-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1209 CCAGTTTCATACTCATGAGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1089 IGAAGTAAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTC 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCAGTITCATACICATGAGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IGCIGAGGACACATIGCAAGCACAAGGAGAGATITCIAATGAIGTGGAAGTGGTGAAAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 394.6; DB 11; Length 1490;
Pred. No. 1.1e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Muscle, rh
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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299 c 328 g
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                                                                                                                                                                                                                                                                                                                                                      http://www.systemsbiology.org
                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3%;
99.0%;
                                                                                                                                                                                                                           Contact: MGC help desk
                                                    (bases 1 to 1490)
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                                                                                             Direct Submission
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                                                           REFERENCE
                                                                               AUTHORS
                                                                                                                        JOURNAL
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                                                                                                                                                                                                               REMARK
                                                                                                                                                                                                                                 COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 784)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,S., Leveloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher
John Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dlone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression
Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
a 183 c 174 g 184 tormal circumstances."
                                               DGZ12445
RST32032 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG212445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1350 GAATATTTCTGACAGAGCAGCCTTT-----GGAAGGACTAGAGAACTCTACCAGG 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1461 AGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGA 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1521 GAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGG 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1581 ACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCC 1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.9%; Score 262.8; DB 12; Length 784;
Conservative 0; Mismatches 287; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AGCAAGTGGACAAGGCATTGGAGAAACTCAGAGACCTGCAGGGAGCTATGGATGATGACTGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 ACGCTGACATGAAGGAGGCAGAGTCCGTGCGAATGGCTGGAAGCCCGTGGGAGACTTAC 360
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3201 Carnegie Ave, Cleveland, OH 44115, USA
                                                                                                                                                                                                                                                                                                                                                                                                  uctivation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: scain@athersys.com
                                                                                                             BG212445.1 GI:13734132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                  DEFINITION
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                                                                                                                                                                             ORGANISM
RESULT 6
BG212445
                                                                                       ACCESSION
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BCUILUBZ 2334 bp mRNA linear HTC 07-AUG-2002 Mus musculus, Similar to utrophin, clone IMAGE:3979320, mRNA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2334)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                1701 CTCTGAAAGAAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCA 1760
                                                                                                                                            1761 ITCAGCICICACCGIATAACCICAGCACTCIGGAAGACCIGAACACCAGAIGGAAGCIIC 1820
                                                                                                                                                                                                                                                                                                                                       Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                           1821 TGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTC 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                      1941 CAAACAAAGTGCCCTACTATATCAACCACGAGAC-TCAAACAACTTGCTGGGACCATCCC 1999
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Series: IRAK Plate: 23 Row: j Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein
This clone has the following problem: incomplete processing.
361 TCATTGACTCGCTGCAGGATCACATTGAAAAATCATGGCATTTAGAGAAGAAATTGCAC 420
                                                                                    421 CAATCAACTTTAAAGTTAAAACGGTGAATGTTTTATCCAGTCAGCTGTCTCCACTTGACC 480
                                                                                                                                                                                        481 IGCAICCTCTCTAAAGAIGTCTCGCCAGCTAGATGACCTTAATAIGCGAIGGAAACTIT 540
                                                                                                                                                                                                                                                                            Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000 AAAATGACAGAGCTCTACCAGTCTTTAGCTGACTGAATAAT 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
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Direct Submission
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/clone="IMAGE:3979320"

DNA Sequencing by: Incyte Genomics, Inc. Constitution information can be Clone distribution: MGC clone distribution

found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM1169 row: column: 16 High quality sequence start: 3 High quality sequence stop: 771.

/organism="Mus musculus"

source

FEATURES

/strain="C57BL/6J

Location/Qualifiers

/db_xref="taxon:10090" /clone="IMAGE:5149431"

Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Contact: Robert Strausberg, Ph.D.

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 CCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCAA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 GATGAATCTAGTGGAGATCACGCAACTGCTGTTGGAAGAACAACTTAAGGTATTGGGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 AGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTG 361
/tissue_type="Mammary tumor, Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Maml"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 ACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGCT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 AATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAA 241
                                                                                                                                                                                                                                                                                                                                             GCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAATGATGTGGAAGTGGTGAAAGAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                122 CAGTITCATACICAIGAGGGGIACAIGAIGGATITGACAGCCCAICAGGGCCGGGIIGGI 181
                                                                                                                                                                                                                                                            602 GATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTACAAGA 657
                                                                                                                                                                           DB 11; Length 2334;
                                                                                                                                                                                                                     .;
                                                                                                                                                                        12 8%; Score 260.8; DB 11; Length 62.3%; Pred. No. 3.2e-52; tive 0; Mismatches 247; Indels
                                                                                          /note="Vector: pCMV-SPORT6"
512 c 638 g 486 t
                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                 409;
                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                 Matches
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/note-"organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,

147 t

243 g

169 c

BASE COUNT

ORIGIN

/clone_lib="NCI_GGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"

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542 GATGAATCTAGTGGAGATCACGCAACTGCTGTTGGAAGAACAACTTAAGGTATTGGGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 CCGCIGGGTGATGACCIGCCCCCCCGGAAGCTGCTICAAGAACAIAAAATTTIGCAA 522
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                                                                                                                                                                                                                                                                                                    223 AGCGTCCTGCAGGCTGGCAACCAGCTGATGACACAAGGACTGACAAGGAGCAGAGGAGC 282
                                                                                                                                                                                                                                                                                                                                                   242 ACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGCT 301
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                                                                                                                                                                       104 GCGGAGGACACGTTCCAGGAGCAAGATGACATTTCTGATGATGTCGAAGAAGTCAAAGAG 163
                                                                                             62 GCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGAC 121
                                                                   1; Gaps
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Query Match 12.3%; Score 252; DB 13; Length 772; Best Local Similarity 62.5%; Pred. No. 3.1e-50; Matches 410; Conservative 0; Mismatches 245; Indels
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BI250598 772 bp mRNA linear EST 17-JUL-2001 602993659F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5149431 5',

BI250598.1 GI:14799101

nouse mouse. Mus musculus

ORGANISM

mRNA sequence.

DEFINITION

RESULT 8 BI250598

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ACCESSION

KEYWORDS

VERSION SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus

NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)

(bases 1 to 772)

REFERENCE AUTHORS Unpublished (1999)

JOURNAL

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/db_xref="taxon:8355"
/clone="XL087e22"
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Contact: Tadasu Shin-i
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                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs r@mail nih,gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 835)
                                                                                                                                         BI553820
601390772F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262209 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1274 AACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGT 1333
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                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1394 TACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGTCACTCGGCTTCTA 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 AAGGAGACACATGCGGCCTTTATGGAAGAGTCTAGGGGGCCCCTACATCTATTCT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 GTGCTGGAGTCAGCCTTCCTGTCCCAGCACCATTGAGGAGTTAGAGGAGCCT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: brain; Vector: pBluescriptR (modified
                      602 GAICGAIGGGCAAACAICIGIAGAIGGACAGAAGACCGCIGGGIICIIIIACAAGA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1%; Score 246; DB 13; Length 835; 60.7%; Pred. No. 9e-49; tive 0; Mismatches 320; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11660 row: p column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="hippocampus"
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_95"
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Location/Qualifiers
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Best Local Similarity 60.79
Matches 504; Conservative
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                                                                                                                                                                          mRNA sequence.
BI553820
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                                                                                           RESULT 9
BI553820
                                                                                                                                                                                             ACCESSION
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KEYWORDS
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1454 CGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGAC 1513
                                                                                             1514 TGGCAGAGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGAT 1573
                                                                                                                                                                                         1574 GAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCGTGGC 1633
                                                                                                                                                                                                                                                                                    1634 GATCTCCTCATTGACTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGA 1693
                                           246 TGGAAGCAGGCGACGGTGGCCAGTGAACTGTGGGAAGTTGACAGCCCGCTGTGTGGAC 305
                                                                                                                                                                                                                                                                                                                                                                                  1694 ATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACT 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1754 ITGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGG 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1814 AAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGC-ATGAAGCCCACAGGGA 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1873 CTTTGGTCCAGCATC-TCAGCACTTTCTTTCCACGTCTGTCC-AGGGTCCCTGGGAGAGA 1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1931 GC-CATCTCGCCAAACAAGTGCCCTACTATATCAACCACGAGACT-CAAACAACTTGCT 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ075057
BJ075057 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL087e22 5', mRNA sequence.
                                                                                                                         486 TTCTCCCCCATGAAAGATGGAGTAAGTTGGTGAATGATCTGGCCCACCAACTTGCCAT 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 TATGATGTGCACTTGTCAATGGAGAATTCCCAGGCCCTGGAACAGATCAACGTCCGATGG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              606 AAACAACTACAGGGGTCAGTTAGTGAGAGGCTTAAGCAGCTCCAAGGATGCCCACCAGGA 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIBB Mochii normalized Xenopus tailbud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1989 GGGACCATCCCAAA-ATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAA 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Xenopus laevis"
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SASE COUNT

ORIGIN

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/note="Organ: nervous_normal; Vector: pucl8; Site_1: Smal; /note="Organ: nervous_normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research)
Profiles into the pucl 18 vector. Reverse transcription of profiles into the pucl 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                      Email: asimpsondiudwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=QV2&t2=QV2-NNOO45-
211200-570-d02&t3=2000-12-21&t4=1)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
\operatorname{Simpson}, A \cdot J \cdot Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            874 TGCCAATGTCCTACAGGATGCTACCCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             934 AAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGT 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 GCAACAGTICCCCCIGGACCIGGAAAGTITCITGCCIGGCTIACAGAAGCIGAAACAAC 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL602076

DKFZp3138029_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp3138029 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.1%; Score 226; DB 12; Length 250; 100.0%; Pred. No. 4.4e-44; tive 0; Mismatches 0; Indels
                                                            Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    994 TIATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTG 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 249.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: puc 18 forward
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                                                                                                                              Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                    Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF963618
QV2-NNO045-211200-570-d02 NNO045 Homo sapiens CDNA, mRNA sequence.
BF963618
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
                                                                         /dev_stage="stage 25" /dev_stage="stage" | Site_1: Not1; Site_2: EcoRI; cDNAs /note="Vector: pBsRN3; Site_1: Not1; Site_3: ctaging
                                                                                                           were oligo-dr primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1902 CCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAGTGCCCTACTATA 1961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1962 TCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGT 2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1602 AGGIGATCAAGGGATCCIGGCAGCCCGTGGGCGAICICCTCATIGACTCTCTCCAAGATC 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1662 ACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCC 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1722 ACGICAAIGACCIIGCICGCCAGCIIACCACIIIGGGCAIICAGCICICACCGIAIAACC 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1782 TCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACC 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1482 AGTGGGAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTG 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1542 AAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTG 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 GICICAAACAACICCAAGAAGCACTIGGGATITIGGACCIGCCICCCAACACITICICI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 CACTGAATGATATGCCCAGTCAGCTTTGTACCTTTGACCTTTGACCTTTGCAAAAACAT 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 AACGAATACGGGGAAGCTGGAAACCTGTAGGAGATCTGTTAATTGATTCCTTGAAGGATC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                       16 AGTGGGACAGCCTGAACTCTCAGGCCAGCAGTTGGCAGAAGCAAGTGGACAAAGCCTTGG 75
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.5%; Pred. No. 9.9e-48;
Matches 361; Conservative 0; Mismatches 199; Indels 0:
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                                               /tissue_type="whole embryo"
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ORGANISM

REFERENCE AUTHORS

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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                           High quality sequence stop: 419.
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%;
                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 364; Conservative
    Gene Index
                                                                                                                                                                                                                                                                                                                     .645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       source
                    JOURNAL
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                 This is the 5' sequence of the clone insert Clone from 5 Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Bmail s. wiemanneGMfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the CDNA sequencing consortium of the
                                                                                                                                            No sI sequence available.
This clone (DKFzp313B029) is available at the RZPD in Berlin.
Phase contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1631 GGCGATCTCCTCATTGACTCTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGA 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1691 GAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACC 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1751 ACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGA 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1811 TGGAAGCTICTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGG 1870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 042)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1871 GACTITIGGICCAGCAICTCAGCACTITCTTTCCACGICTGTCCAGGGICCCTGGGAGAA 1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1931 GCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACAACTTGCTGG 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GAAATTGCACCAATCAACTTTAAAAGTTAAAACGGTGAATGATTTATCCAGTCAGCTGTCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCACTTGACCTGCATCCCTCTCTAAAGATGTCTCGCCAGCTAGATGACCTTAATATGCGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 10.3%; Score 209.4; DB 9; Length 5 al Similarity 69.3%; Pred. No. 5.7e-40; 285; Conservative 0; Mismatches 126; Indels
Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                         /clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 t
                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                     /clone="DKFZp313B029"
                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 g
                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA-collection"
125 c 86
                                                                                                                            German Genome Project
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Query Match Best Local Matches 28

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BASE COUNT

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FEATURES

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Email: cgapbs remail.nih.gov
Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center.
Clone distribution: NCI-CGAP_clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:2920478"
/clone_lib="NCI_CGAP_CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rearrangement positive, includes both chronic phase and myeloid blast crisis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    959 GACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGC 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1019 CAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTG 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1079 GATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAGTCTCTCAACATTAGGTCCCAT 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1139 TIGGAAGCCAGTICIGACCAGIGGAAGCGICIGCACCTITCICIGCAGGAACTICIGGIG 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1199 TGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCA 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   839 AAGTITCTIGCCIGGCITACAGAAGCIGAAACAACIGCCAAIGICCIACAGGAIGCIACC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 645 AACTICCIGAAGIGGAICCAAGAAGCAGAGACCACACAGIGAAIGIGCIIGIGAAIGCCICI 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            899 CGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAA 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 CATCGGGAGAATGCTCTTCAGGATAGTATCTTGGCCAGGGAACTCAAACAGCAGATGCAG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        465 CAGAAGAIGGIAAAAGCIIIGGGAAAIICTGAAGAGGCIACIAIGCIICAACAICGACIG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1259 GCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAA 1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1319 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTT---- 1374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 TATTCTGTCCTGAATGCTGTCGACCAGGCCCGAGTTTTCTTGGCTGATCAGCCAATTGAG 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 182.4; DB 10; Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.1e-33;
0; Mismatches 272; Indels
                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
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DEFINITION

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KEYWORDS

ORGANISM

REFERENCE AUTHORS JOURNAL MEDLINE

COMMENT

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The sequence contained an oligo-dr track that was present in the oligonic contained an oligo-dr track that was present in the strand closed that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NOTI site and the oligo-dr track served to identify it as a clone from the normalized rat placenta pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-21, >AT_rich#Low_complexity Seq primer: M.3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-uvector: pt713D-Pac (Pharmacia) with a modified /note-"vector: pt713D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; The UI-R-DKO library is a subtracted library derived from a mixture of five individually tagged normalized rat libraries: brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP (20%), and placenta-nRPP (20%). Each original aorta-nRPP (20%), and placenta-nRPP (20%).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 19-JUL-2001
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 646)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646 bp mRNA linear EST 19-JUL-2
UI-R-DKO-cfe-e-07-0-UI.S1 UI-R-DKO Rattus norvegicus CDNA clone
RI2R-DKO-cfe-e-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7Fel: 319 335 9565 Fax: 319 335 9565
                                                                                                                                                                                                                                                                            1956 ACTATATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCT 2015
                                                    1836 AGGACCGAGTCAGCAGCAGCATGAAQCCCACAGGACTTTGGTCCAGCATCTCAGCACT 1895
                                                                                                                                                                152 AGATGTCTCGCCAGCTAGATGACCTTAATATGCGATGGAAACTTTAACAGGTTTCTGTGG 211
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/lab_host="DH10B (Life Technologies)"
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Program for Rat Gene Discovery and Mapping
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/clone_lib="UI-R-DK0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome_Res. 6 (9), 791-806 (1996)
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-BT0634-
290800-346*bl2&t3=2000-08-2844*1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence start: 25
High quality sequence stop: 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, D.F., de Souza, S.J. and
                                                                                                                                                                                                                                                     EST 16-MAY-2002
                                                                                                                                                                                                                                                     BQ304046
QV2-BIO634-290800-346-b12 BT0634 Homo sapiens CDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 5.6e-32;
0; Mismatches 131; Indels 0;
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                                                          1430 GCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTC 1474
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Best Local Similarity 66.1%;
Matches 255; Conservative (
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FEATURES

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eminaryoutc. scages). Each indicty was normalized individually according to the procedure described by Bonaldo. Lennon & Soares (Genome Research Genome 6: 791-80. 1966). For construction of the five individually specified above and electroporated into competent bacteria for production of single-stranded circular DNA crepresenting the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hypitalization template preparation) comprising; a) a set of about 1,000 libraries of brain (CTOs), heart (CSOs), kidney (CUOs), approximately 5,000 clones represented about 2,000 arrayed clones from each of the five non-normalized aorta (CTOs), heart (CSOs), kidney (CUOs), approximately 5,000 clones represented about 2,000 arrayed clones from each of the five normalized clones from each of the five normalized or clones from each of the five normalized about 2,000 arrayed clones from each of the five normalized or clones from each of the five normalized about 6.000 clones rate. CCTO). The resulting pool of about 10,000 clones from each of the final driver population.
RNA from seven different developmental time-points: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult day 12, adult day 75, and adult day 200. (Exception: the aorta pool does not contain embryonic embryonic stages). Each library was normalized
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TAG_TISSUB=rat placenta pool
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DB 13; Length 646; 1 others 198 t 8.2%; Score 167.2; 50.1%; Pred. No. 1e-129 g TAG_SEQ=TCACGACAGT" Similarity 131 Query Match BASE COUNT ORIGIN

197 GGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAG 256 639 GGCAACCAACTGATGACACAAGGCACTCTGTCGGATGAGGAGGAGTNTGAGATTCAGGAG 580 Gaps 184; Indels le-29; 60.1%; Pred. No. Matches 277; Conservative οy δy

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459 TGGCTGACCTCACAGAGGAGCGCATTCAGAAGATGGAAAGCCTCCCAGTGGGTGACGAC 400

437 CTTGAAGACCTAAAACGCCAAGTACAACATAAGGTGCTTCAAGAAGATCTAGAACAA 496

497 GAACAAGTCAGGGTCAATTCTCTCACTCACATGGTGGTGGTAGTTGATGATCTAGTGGA 556

557 GATCACGCAACTGCTGTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGCAAAC 616

617 ATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGA 657

219 GTATGCCGCTGGACTGAAGAACGTTGGAACAGGTTGCAAGA 179

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Search completed: April 25, 2003, 17:37:52 Job time : 1944.12 secs

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                                                                                                                                                                                                                                                                                                                                                                              Description
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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5210183-1
US-08-83-1
US-08-9-007-005-17
US-09-24-796-17
US-09-014-959-14
US-08-630-915A-193
US-08-4139-937-12
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                                                                                                                                             441362 seqs, 153338381 residues
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Maximum Match 100%
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Sequence 5, Appli Sequence 44, Appl Sequence 43, Appl Sequence 189, App Sequence 187, App Sequence 187, Appl Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 184, Appli Sequence 184, Appli Sequence 184, Appli Sequence 184, Appli Sequence 184, Appli Sequence 184, Appli Sequence 370, Appli					VACCINE																						
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33 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		7-073-4 ce 4, Applica	GENERAL INFORMATION: APPLICANT: Paolet	LICANT: de 1 LICANT: Tine	TITLE OF INVENTION: MAI NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:	ODRESSEE: Cu	TY: New YOR	DUNTRY: UNIT	UTER READABL	DIUM TYPE; MPUTER: IBM	FIWARE: Date	ENT APPLICAT	LING DATE:	CLASSIFICATION: 424 PRIOR APPLICATION DATA:	PLICATION NUP LING DATE:]	PRIOR APPLICATION DATA APPLICATION NUMBER	FILING DATE: 18-MAR-19	APPLICATION NUMBER	ALNG DATE: 2	4E: Frommer,	REFERENCE/DOCKET NUMBER: 4	TELEPHONE: (212) 840-3	EX: 425066	CRMATION FOR SEQ ID NO SEQUENCE CHARACTERISTIC	2223 cleic	TOPOLOGY: lines	
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REGISTRATION NUMBER: 28,977
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INFORMATION FOR SEQ ID NO: 3:
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nucleic acid
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                           348 AGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAAAAGAAGGA 407
                                                                                                                            408 AAATGGAGGAAGAGCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAC 467
                                    Gaps
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44.0%; Pred. No. 0.14;
tive 0; Mismatches 209; Indels 0;
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Query Match 2.0%; Score 40.4; DB 1; Length 2223; Best Local Similarity 51.7%; Pred. No. 0.042; Matches 92; Conservative 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1447-106P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08425069 Patent No. 5728810
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NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lewis, Randolph V. APPLICANT: Xu, Ming APPLICANT: Hinman, Michael B.
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TELEFAX: (703) 205-8050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1995 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 22046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virginia
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
US-08-425-069-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                         US-08-425-069-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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APPLICANT: Lewis, Randolph V.

APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       971 TAGGAGGITATGGACCAGGACAACAAGGTCCAGGAGGATATGGACCAGGACAACAAGGTC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1559 CAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCC 1618
                                                                                                                                                                                                    1439 GTCACTCGGGTTCTACGAAAGCAGGCTGAGGGGTCAATACTGAGTGGGAAAATTGAAC 1498
                                                                                                                                                                                                                                                                                                                                                                                                         1499 CTGCACTCCGCTGACTGGCAGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTT 1558
                                                                                                   1319 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA 1378
1259 GCAGTTCAGAAGCAAGGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAA 1318
                                                                                                                                                                                                                                                                                                                                                        911 GACCATCTGGAGCAGGCAGTGCAGCAGCAGCGCGCAGCAGGACCTGGACAACAAGGAT 970
                                                                                                                                                    791 cagacaacaacaarcrigaacccggragreccgcriccacagcagcagccgccacag 850
                                                                                                                                                                                                                                    731 GCAGTGCAGCTGCAGCAGCAGCAGCAGCACCTGGACAACAAGGACCCGGAGGATATGGAC 790
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APPLICATION NUMBER: US/08/317.844R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOMBER OF CASE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
STATE: Virginia
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1259 GCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAA 1318
                                                                                                                                                                                                                                             1319 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA 1378
                                                                                                                                                                                                                                                                                                             1439 GTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAAC 1498
                                                                                                                                                                                                              731 GCAGTGCAGCTGCAGCAGCAGCAGCAGCACCTGGACAACAAGAACCGGGAGGATATGGAC 790
                                                                                                                                                                                                                                                                   1499 CTGCACTCCGCTGACTGGCAGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTT 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               971 TAGGAGGTTATGGACCAGGACAAGGTCCAGGAGGATATGGACCAGGACAACAAGGTC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1559 CAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCC 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    911 GACCATCTGGAGCAGGCAGTGCAGCAGCAGCGCGGAGCAGGACCTGGACAAGGAT 970
                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 AAAAAGTTAGACGAAGATAATGCTAAACTTGTTGAGGTTGTTGAAACCACAAGTTTGGAA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 AACGAAAAACTCAAGAGTGAGAATGAGGAATAAGAAAATTTAGACAAAACTTAGCAAA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 GATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAAAAGAAGAAGA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 ACAAGGAAAATGGAGGAAGGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                 1.9%; Score 38.6; DB 2; Length 1995;
44.0%; Pred. No. 0.14;
tive 0; Mismatches 209; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 45.9%; Pred. No. 0.13;
Matches 130; Conservative 0; Mismatches 153; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5180810

APPLICANT: Gomi, Hideyuki, Hozumi, Tatsunobu, Hattori, Shizuo, Tagawa, Chiaki, Kishimoto, Fumitaka, Bjorck, Lars, TITLE OF INVENTION: PROTEIN H CAPABLE OF BINDING TO IGG CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/376,641

FILING DATE: 07-JUL-1989
                                                                                                                               Local Similarity 44.0° tes 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1619 TGGCAGCCCGTGG 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1091 AAGGACCAGGAGG 1103
                                                                     1..1785
IMMEDIATE SOURCE:
                                               ; NAME/KEY: CDS
; LOCATION: 1..1
US-08-317-844B-3
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                                                                                                                                               Matches 164;
               CLONE:
FEATURE:
                                                                                                                 Query Match
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221 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 AACGAAAAACTCAAGAGTGAGGAGAGAATAAGAAAATTTAGACAAACTTAGCAAA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 GATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAAACAGAAGAAGA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 GAAAATCAAGGAAAAGCTCGAAAAATTGGAGCTTGACTATCTCAAAAATTAGATCACGAG 663
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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45.9%; Pred. No. 0.18;
tive 0; Mismatches 153; Indels 0,
                                                                                                                                                       APPLICANT: Gomi, Hideyuki; Hozumi, Tatsunobu; Hattori, Shizuo; Tagawa, Chiaki; Kishimoto, Fumitaka; Bjorck, Lars TITLE OF INVENTION: PROTEIN H CAPABLE OF BINDING TO IGG CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 07-JUL-1989
461 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAAG 503
                       397 TTAGAACGTAAATACCAACGAGAAGTAGAAAAGGTTATCAAG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAAGA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       724 TTAGAACGTAAATACCAACGAGAAGTAGAAAAGGTTATCAAG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Bouguelerert, Lydie TITLE OF INVENTION: Complementary DNAS FILE REFERENCE: GENSET.021A CURRENT APPLICATION NUMBER: US/09/247,155A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1999-02-09
EARLIER PILING DATE: 1999-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 76, Application US/09247155A ; Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                   5180810-2
;Patent No. 5180810
                                                                                                                                                                                                                                                                                                                          LENGTH: 1784
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                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 AGAACGTGAAAAATATCTATCTTATGCTGACGATAAAGAAAAAGATCCTCAATCTAGAGC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 TTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 ATTAATGGGTGAAAATCAAGATCTTCGAAAAAGAGGGGGGACAATATCAGGACAAAATAGA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 AGCGTGGAACTGGCCTAAAGAATATAACGCGTTACTTAAGGAAAATGAGGAGCTCAAGGT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 TTCAAGATGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                        1087 AAAAACAATTTAAAATTTCAAATTTTAAAATTGCTGCACCATAAGATGAATAAAGGC 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 AACAGGAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAA 273
                                                                                                                                                                                                                                                                                                                                                                                            309 AAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGT 368
                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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nllarity 45.5%; Pred. No. 0.5;
Conservative 0; Mismatches 157; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE NO. 5210183
PRICANT: LINDAHL, GUNNAR; FRITHZ, ELISABET; HEDEN, LARS-OLOF
TITLE OF INVENTION: PROTEIN ARP, WITH IMMUNGLOBUIN A
BINDING ACTIVITY, THE CORRESPONDING VECTORS AND HOSTS, REAGENT
KIT AND PHARMACEUTICAL COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 TGAATGACTGGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9%; Score 38; DB 4; Length 1394;
59.1%; Pred. No. 0.17;
tive 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 CCAAGTACAACAAAAGGTGCTTCAAGAAGATCTAGAACAAGAACA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide
LOCATION: 46..87
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LTLLGLSLILAGL/IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPLICATION NUMBER: US/07/270,099
FILING DATE: 14-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 186,097
FILING DATE: 25-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           0.0ery Match
Best Local Similarity 59.19
Matches 65; Conservative
                                                                                                                                                                        NAME/KEY: polyA_signal
LOCATION: 1363..1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                    ; NAME/KEY: polyA_site
; LOCATION: 1382..1394
US-09-247-155-76
LOCATION: 46..675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5210183-1
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US-08-887-534A-22

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330 GAGTITTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAA 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 TIGGAACAGGAAAATTAICAGAAGAIGAAGAACTGAAGTACAAGAGCAGAIGAATCTCC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 TAAAITCAAGAIGGGAAIGCCICAGGGIAGCTAGCAIGGAAAAACAAAGCAATITACAIA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 AAATCGTCAACTTGGATGGGCTACAACTATCCTTCACGATTAAAGATAGTGATTTTCATC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 TGGATITGACAGCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 TGGCTTTGGATAAACATATGATGCATGTAACAATTAGTTATCCCCTACCTGACAATCAGC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.6; DB 4; Length 1845;
Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score ov.v.,
48.0%; Pred. No. 0.57;
vive 0; Mismatches 144; Indels
Sequence 22, Application US/08887534A
Patent No. 6455323
GENERAL INFORMATION:
APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                               E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 CAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGA 430
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                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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DESCRIPTION: /desc = "DNA (genomic) (p14c15)"
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT IREORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 28341/33996
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELERAX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            US/08/887,534A
                                                                                                                                                                                                             United States of America
                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 48.0°
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 856..1842
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
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                                                                                                                                                                                  COUNTRY: Unit-
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                                                                                                                                                                                Chicago
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                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                  STREET:
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Patent No. 625858
GENERAL INPORMATION:
APPLICANT: SCOSTAK, Jack W.
APPLICANT: ROBETS, Richard W.
APPLICANT: LANDERSON SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: 108108
FILE REPRESENCE: 00786/35003
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1997-11-06
SOFTWARR: FASTSEQ for Windows Version 4.0
ELECTHIC 289
LENGTH: 289
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Patent No. 6281344
GENERAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: SZOSTAK, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
ITILE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SOUSONS
FILE REPERRNE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER PPLICATION NUMBER: 60/064,491
EARLIER PILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 00/064,491
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER PILING DATE: 1998-11-06
EARLIER PILING DATE: 1998-01-14
SOFTWARE: FastSEQ for Windows Version 4.0
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1.8%; Score 36.2; DB 4; Length 289;
Best Local Similarity 6.1%; Pred. No. 0.21;
Matches 14; Conservative 99; Mismatches 118; Indels (
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    LOCATION: (1)...(289)
    OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
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282 GGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGG 341
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APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 1.8%; Score 36.2; DB 4; Length 2 Best Local Similarity 6.1%; Pred. No. 0.21; Matches 14; Conservative 99; Mismatches 118; Indels
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APPLICATION NUMBER: US/09/01/ 0.7
                                                        FEATURE:
OTHER INFORMATION: Translation template
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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Patent No. 5965397
GENERAL INFORMATION:
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APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 41,323
TELEPHONICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
FORMATION FOR FIGURE AND FOR FIGURE AND FIGURE
ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO: 14:
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REGISTRATION NUMBER: 41,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 2447 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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APPLICANT:
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RESULT 14
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APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: McCONNELL, Stephen J.
APPLICANT: McCONNELL, Stephen J.
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                              304 CAIGGAAAAACAAAGCAAITIACAIAGAGITIITAAIGGAICICCAGAAICAGAAACIGAA 363
                                                                                                                                                                                                                                         244 TGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGCTAG 303
                                                                                                                                                            184 TATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAAAC 243
                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   364 AGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAA 418
                                                                                 Query Match 1.8%; Score 36.2; DB 2; Length 2447; Best Local Similarity 46.8%; Pred. No. 0.92; Matches 110; Conservative 1; Mismatches 124; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Pennie & Edmonds LLP
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03-APR-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; sequence 193, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 16,872
REFERENCE/DOCKET NUMBER: 1101--
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
TELEFAX: (612) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DC TITLE OF INVENTION: DC TITLE OF INVENTION: US NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2873 bases
STRANDEDNESS: double
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                               MOLECULE TYPE: CDNA
JS-09-014-969-14
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                    TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 AAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                 413 GAGGAAGACCTCTTGGACCTGATCTTGAAGACCTAAAACGCCCAAGTACAACAACATAAG 472
                                                                        42 CAGAAAAAGAAACTAGAAGAAGATGCAAGGAAAGCAAAGGAAAGGAAAAGAAAAGTTA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 1.8%; Score 35.8; DB 4; Length 790; I Similarity 61.1%; Pred. No. 0.56; 58; Conservative 0; Mismatches 37; Thable
1.8%; Score 36; DB 4; Length 2873; 52.7%; Pred. No. 1.2; tive 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 CTGGCTAACAAAACAGAAGAAGAACAAGGAAAA 410
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APPLICANT: Sakai, Hajime
FILE REPERENCE: BB1303 US NA
CURRENT APPLICATION UNDHER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER PPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE
                                                                                                                                                                                                                                     473 GTGCTTCAAGAAGATCTAGAACAAGAAC 500
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08139937
Patent No. 5821070
                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09461474
Patent No. 6728042
GENERAL INFORMATION:
APPLICANT: Allen, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Triticum aestivum
US-09-461-474-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LEE, WEN-HWA APPLICANT: SHAN, BEI
          Query Match
Best Local Similarity 52.7%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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LENGIH: 790
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                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-461-474-13
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384 CAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAG 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application PC/TUS9311310
GENERAL INFORMATION:
APPLICANT: BOARD OF RECENTS OF THE UNIVERSITY OF TEXAS SYSTEM
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.9%; Pred. No. 2.3;
Matches 80; Conservative 0; Mismatches 74; Indels 0
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/11310
FILING DATE: 19-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2041 TGAAAGAAAATCAAGCACTGCCATGGAGATGCT 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 TCAGGGTCAATTCTCTCACATGGTGGTGGT 537
                                             FILING DATE: 20-0CT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/979,156
FILING DATE: 20-NOV-1992
ATTORNEY, AGENT INFORMATION:
NAME: CAMPBELL, CATHREY
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 9370
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,937
FILING DATE: 20-007-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CAMBBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: FP-CJ 9790
                                                                                                                                                                                                                                               TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
                                                                                                                                                                                                                                                                                                    LENGTH: 4868 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-535-8949 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                       TELEPHONE: 619-555-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ; STRANDEDNESS: sing; TOPOLOGY: linear; MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALIFORNIA
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SOFTWARE:
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384 CAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAG 443
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                                                                                                                                                         0; Gaps
                                                                                                                1.7%; Score 35.6; DB 5; Length 4868;
51.9%; Pred. No. 2.3;
itive 0; Mismatches 74; Indels 0
                                                                                                                                                                                                                                                                                                        2041 TGAAAGAAAATCAAGCACTGCCATGGAGATGCT 2074
                                                                                                                                                                                                                                                                                       504 TCAGGGTCAATTCTCTCACTCACATGGTGGTGGT 537
                                                                                                                                                                                                                                                                                                                                                               Search completed: April 25, 2003, 17:43:03
Job time : 76.4852 secs
            LENGTH: 4868 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                                                          80; Conservative
                                                                          CDNA
                                                                                                             Query Match
Best Local Similarity
                                                           linear
                                                   ; TOPOLOGY: lin
; MOLECULE TYPE:
PCT-US93-11310-12
                                                                                                                                              Matches
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(without alignments)
16376.941 Million cell updates/sec
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Sequence 27715, A
Sequence 21956, A
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Sequence 183, App
Sequence 183, App
Sequence 183, App
Sequence 183, Sequence 183, App
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Sequence 10742, A
Sequence 18355, A
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Sequence 204, App
Sequence 12395, A
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App
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                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 183,
Sequence 183,
                                                                                      April 25, 2003, 17:39:49 ; Search time 135.61 Seconds
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Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            'cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
'cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
'cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
'cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
'cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
'cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-960-352-10742
US-09-864-761-18355
US-09-960-352-4010
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US-09-864-761-27715
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US-09-960-352-12395
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US-10-175-752-183
US-10-176-482-183
US-10-176-757-183
US-10-176-913-183
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US-10-174-590-183
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                                                                                                                                                                                                                                                         709820 seqs, 544064369 residues
                                                                                                                                                 US-09-845-416-6_COPY_1020_3060
                                                   OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_NA:*
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Listing first 45 summaries
                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 5000
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2.1
2.0
1.9
1.9
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Sequence 183, App
US-10-180-552-183 US-10-173-700-183 US-10-174-572-183 US-10-174-572-183 US-10-174-582-183 US-10-175-739-183 US-10-175-739-183 US-10-175-739-183 US-10-175-739-183 US-10-175-740-183 US-10-176-781-183 US-10-176-781-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-991-183 US-10-176-981-183 US-10-176-981-183 US-10-178-681-183 US-10-178-681-183
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENONE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HILE REFERENCE: Accomica-Y-1
CURRENT APPLICATION UNMER: US
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-37
PRIOR FILING DATE: 2000-06-37
PRIOR FILING DATE: 2000-06-37
PRIOR FILING DATE: 2000-09-37
PRIOR FILING DATE: 2001-01-37
PRIOR FILING DATE: 2001-01-37
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
ALIGNMENTS
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                               Sequence 11083, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                     US-09-864-761-11083
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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7.4%; Score 151; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 151; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96
CTHER INFORMATION: EXPRESSED IN BOWE MARROW, SIGNAL = 0.81
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81
OTHER INFORMATION: WISSPROT HIT: P11532, EVALUE 4.00e-08
USHER INFORMATION: SWISSPROT HIT: P11532, EVALUE 4.00e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27715
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              PRIOR APPLICATION NUMBER: PCI/USOL/VOOGS PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21 PRIOR PILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: US 09/774,203
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-26
PRIOR FILING DATE: 2000-08-03
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Patent No. US20020048763A1
PRIOR APPLICATION NUMBER: PCI/US01/00665
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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US-09-864-761-21956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 GCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 CAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTG 378
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                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN LIVE, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81
US-09-864-761-11083
                               PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PRILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOGTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11083
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CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-37
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-10-37
PRIOR FILING DATE: 2000-10-37
PRIOR FILING DATE: 2000-10-37
PRIOR FILING DATE: 2001-130
PRIOR FILING DATE: 2001-130
PRIOR FILING DATE: 2001-130
PRIOR FILING DATE: 2001-130
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
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; Patent No. US20020048763A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: GB 24263.6

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGCTGAGGACACATTGCAAGGACACAAGGAGATTTCTAATGATGTGGAAAGTGGTGAAAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO ACGO4468.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEO ID NOS: 49117
SOFTWARRE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                               CURRENT FILLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 05 60/180,312
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-08-03
PRIOR FILLING DATE: 2000-09-03
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2001-01-09-27
PRIOR FILLING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
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PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                             FILE REFERENCE: Aeonica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
                                               Rank, David R.
Hanzel, David K.
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Matches 124; Conservative
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                                         APPLICANT:
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97.9%; Pred. No. 5.7e-32;
tive 0; Mismatches 3; Indels 0;
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OTHER INFORMATION: EXPRESED IN PLACENTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESED IN BRAIN, SIGNAL = 1.7

OTHER INFORMATION: EXPRESED IN BRAIN, SIGNAL = 1.7

OTHER INFORMATION: EXPRESED IN ADULT LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESED IN HELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESED IN FIRSTAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESED IN FIRSTAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: SWISSPROT HIT: P11532, EVALUE 2.00e-30
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PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-06-30
PRIOR PAPLICATION NUMBER: US 09/608,408
PRIOR PAPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                     PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRING APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-864-761-18355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 18355
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Sequence 1835, Application US/09864761
Sequence 1835, Application US/09864761
Sequence 1835, Application US/09864761
Sequence 1835, Application US/088476341
SEQUENCEMENT Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: HUMAN GENOME-2.23
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                       PARENT NO. 022022

PAPENT NO. 022022

APPLICANT: Wasley C.
APPLICANT: Byat. John C.
APPLICANT: Byat. John C.
APPLICANT: Byat. John C.
APPLICANT: Wathialagan, Wagappan
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10299)C
CURRENT APPLICANTON WHERE: US/09/9660,352
CURRENT APPLICANTON WHERE: US/09/9660,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10742
LENGTH: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1%; Score 43; DB 10; Length 436; Best Local Similarity 48.6%; Pred. No. 0.017; Matches 118; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bos taurus
ORGANISM: Bos taurus
ORGANISM: OTHER INFORMATION: Clone ID: 46-LIB3058-032-Q1-K1-D10
US-09-960-352-10742
                                                                                                                                                                                                                                   Sequence 10742, Application US/09960352 patent No. US20020137139A1
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395 GAAAGAACAAGGAAAATGGAGGAAGGACCTCTTGGACCTGATGTTGAAGACCTAAAAGGC 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 51.2%; Pred. No. 0.029; Similarity 51.2%; Pred. No. 0.029; 18; Conservative 0; Mismatches 138; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: MAP TO ACO10133.1

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN BOLE ARROW, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN BONE WARROW, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEARIN, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN PLACEWIR, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN PLACEWIR, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BTA74, SIGNAL = 2.2
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/USO1/00668 PRIOR FILING DATE: 2001-01-30 PRIOR PLICATION NUMBER: PCT/USO1/00663 PRIOR FILING DATE: 2001-01-30 PRIOR PLING DATE: PCT/USO1/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00670
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
                                                                                PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICANT: Tao, westey C.

APPLICANT: Bydtt, John C.

APPLICANT: Mathialagan, Nagappan

TILLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND CURRENT APPLICATION NUMBER: 16511.006/37-21(10299)C

CURRENT APPLICATION NUMBER: US/09/966,352

NUMBER OF SEQ ID NOS: 15112

LENGTH. 12355
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53.1%; Pred. No. 0.1;
tive 0; Mismatches 76; Indels 0
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47.1%; Pred. No. 0.15;
tive 0; Mismatches 137; Indels 0;
                                                                                                                                                                                                                                                              378 GGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAG 419
                                                                                                                                                                                                                                                                                   328 GGACTCAAAAATTAATGTGTCCAACAGAAGAATGGAAG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Glone ID: 53-LIB3058-009-Q1-K1-F2 US-09-960-352-12395
                                                                                                                                                                                                                                                                                                                                                                Sequence 12395, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 343, Application US/09822846 ; Publication No. US20030027139A1
                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 ACAACAACATAAGGTGCTT 478
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22; Conservative
                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                US-09-960-352-12395/c
                                                     US-09-864-864-204
            LENGTH: 428
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                                                                                       Query Match
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                                                     GENERAL INCORACTOLIS/139A1
GENERAL INFORMATION:
APPLICANT: Warten, Wesley C.
APPLICANT: Taro, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUCLEIC ACID AND DEPOSITION
TITLE OF INVENTION: MUCLEIC ACID AND DEPOSITION
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND CURRENT APPLICATION WUMBER: US/09/960,352
CURRENT APPLICATION WUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                       220 AAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAG 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Benson, Darin R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 ACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAAGAAGTCA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 18-BOVMS1-007-01-E1-E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 210121.535 CURRENT APPLICATION NUMBER: US/09/864,864 CURRENT FILING DATE: 2001-05-23 NUMBER OF SEQ ID NOS: 341 SOFTWARE: Corixa Invention Disclosure Database SEQ ID NO 204
RESULT 7

78-09-960-352-4010/c

5 Sequence 4010, Application US/09960352

Fatent No. US20020137139A1
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Patent No. US20020102679A1
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Dillon, Davin C.
APPLICANT: Secrist, Heather
APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                        Matches 133; Conservative
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Fling, Steve P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mannion, Jane
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ORGANISM: Homo Sapien
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US-10-176-758-183/c
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US-10-174-590-183
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: CALCULAR INSTITUTE INC.
APPLICANTON: GENETICAS INSTITUTE APPLICANTON: POLYMUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2000-03-29
PRIOR PELICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                Agostino, Michael J.
Steininger II, Robert J.
Bowman, Michael R.
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                              APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Gulukota, Kamalakar
Graham, James R.
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APPLICANT: Chen, Jian
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Clark, Hilary
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Merberg, David
Treacy, Maurice
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US-09-822-846-343
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                                       GENERAL INFORMATION:
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                                                                                                1281 AAAAACAATTTAAAATTTTAAAATTTTAAAATTGCTCCACATAAGATGAATAAAGAGC 1222
                                                                 309 AAAAACAAAACTTTACATAGACTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGT 368
1.9%, Score 39.6; DB 9; Length 1594;
60.0%; Pred. No. 0.43; 44; Indels 0; Gaps
tive 0; Mismatches 44; Indels 0; Gaps
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CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 183
LENGTH: 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 183, Application US/10175737 ; Publication No. US20030013153A1
                                                                                                                                                                                                                                                                Sequence 183, Application US/10176758; Sequence 183, Application No. US20030008353A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William I.
Zhang, Zemin
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APPLICANT: Baker, Kevin P.
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Gurney, Austin L.
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Smith, Victoria
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Goddard, Audrey
                                                      66; Conservative
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ORGANISM: Homo Sapien
US-10-176-758-183
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Best Local Similarity
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 93430R1C50 CURRENT APPLICATION NUMBER: US/10/175,737 PRIOR APPLICATION DATE: 2002-06-19 PRIOR APPLICATION Temoved - See File Wrapper or Palm
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P34.30 RICT
CURRENT APPLICATION NUMBER: US/10/173,706
Prior Application removed - See File Wrapper or Palm
SET APPLICATION OF SEQ ID NOS: 612
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60.0%; Pred. No. 0.43;
ative 0; Mismatches 44; Indels 0; Gaps
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1 Similarity 60.0%; Pred. No. 0.43;
66; Conservative 0; Mismatches 44; Indels 0;
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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Matches 66; Conservative
     Zhang,Zemin
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US-10-175-737-183
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Best Local Similarity
Matches 66; Conserva
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US-10-173-706-183
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                                                                                                                                SEQ ID NO 183
LENGTH: 1594
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JS-10-175-738-183/C
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LENGTH: 1594
APPLICANT:
                                                                                                                                                                     TYPE: DNA
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APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gunney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/175,738
CURRENT PILING DATE: 2002-06-19
Prior application removed - See File Wrapper or Palm

WUMBER OF SEQ ID NOS: 612
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                      APPLICANT: Baker, Kevin p.
                                                 Chen,Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-738-183
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GENERAL INFORMATION:
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April 25, 2003, 07:56:07 ; Search time 4707.23 Seconds (without alignments) 17070.103 Million cell updates/sec
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Listing first 45 summaries
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 $Pred.\ No.\ is\ the\ number\ of\ results\ predicted\ by\ chance\ to\ have\ a$

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	E30219 Shortened d E30220 Shortened d E30221 Shortened d E30218 Shortened d AF339031 Danio rer M37645 Torpedo cal	M18025 Mouse dystr X83506 M.musculus E30223 Shortened d AF19578 Rattus no AF195787 Rattus no U43519 Human dystr X06179 Human detal M92650 Human Duche BC028720 Homo sapi E30222 Shortened X69767 R.norveqicu	AJ22356 Strongylo X99700 X.laevis mR AF33002 Danio rer X99701 S.caniculua L05649 Homo sapien BC024140 Mus muscu X65468 R.norvegicu AB011666 Rattus no X06178 Human adult U43517 Scyliorhinu M86889 H.sapiens d	AX107969 Sequence AX107970 Sequence AF213410 Homo sapi X99703 C.caniculua AF213411 Homo sapi X66203 Human Duche S62620 (mdx3cv)=dy M2351 Human Duche U43518 Goblus sp. L05647 Homo sapien L043520 Mus musculu AF213440 Homo sapien S38776 Homo sapien S38776 Homo sapien S38776 Homo sapien	linear PAT 18-JUN-2001
SUMMARIES	B30219 B30220 B30221 B3021 B30218 AF339031 FSCDXSIRO	MUSDYS MAGUTRPH E30223 AF195788 AF195787 AF195787 HSDMDF1 HSDMDF1 HSDMDF1 BC028720 E30223	ALDYSTROP AR139032 SCDYSTROP HUMDYSTRI5 BC024140 RNADYI AB011666 RNADXI AS01167 RNADXI AUSMDA1 SCU43317 HUMDYSTROP	AX107970 AX107970 SCUTROPHI AF213401 AF213408 HSDMD S62620 HUMDWBEE GSU4518 HUMDYSTR13 MM43520 AR713440 HUMDYSDMD S38776 PSDYSTR0P	ALIGNMENTS dystrophin. 4402 bp DNA GI:13017026 ted. ed. ed. ed. ed. 1 1 to 4402) dystrophin 1999; TECH AGENCY, NATIONAL CENTER OF
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                                                                                                                                                                  Query Match 46.4%; Score 1281; DB 6; Length 4402; Best Local Similarity 73.4%; Pred. No. 0; Matches 2026; Conservative 0; Mismatches 0; Indels 735.
                                                                                                  /organism='Unidentified'
                                                                            Location/Qualifiers
1. .4402
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                                                                                                                             /organism="unidentified"
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                                                               Strandedness: Both;
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                                                        901 GCCICITGGACCTGAICTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 960
                                      781 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 840
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1861 AAAAATAGAIGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 1920
            1921 CCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCT 1980
                                                          1981 CATTGACTCTCTCCAAGATCACCTCGAGAAGTCAAGGCACTTCGAGGAGAAATTGCGCC 2040
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Shortened dystrophin. E30220 E30220.1 GI:13017027 JP 1999318467-A/3.

E30220

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Patent: 19 1999318467-A 3 24-NOV-1999;
SCIENCE & TECH AGENCY,NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
OS Unidentified
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                                                                                                                                                                                                                                                                                                                                                64; Indels 735; Gaps
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                                                                                                                                                                                                                           'organism='Unidentified'.
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Local Similarity 71.1%; Pred. No. 3.6e-291;
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Strandedness: Both;
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24-NOV-1999
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                                    (bases 1 to 4402)
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unidentified
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                                           Sinichi, T.
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           ORGANISM
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ق	1335 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCCATCAGGGCCGGGTTGG 1394
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a ¥	AGIALICIA AGAGAGAGA GARGA AGAGA AGATA CA AGATA GA ACTGA AGATA CA GAAGA AGA AGA AGA AGA AGA AGA AGA A
ð	SAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC
λζ - (781 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 040
λō	841 GAAAG
qa	75 GAAAGAGTIGAATGACTGGCTAACAAAAACAAAAAAAAAA
oy da	9
7 4	961 AG
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g ò	GATGAATCTAGGGGAAACATCTGTAGATGGACGAAAGACCGGGTTCTTTACAAGACCAC 114 GATCGATGGGCAAACATCTGTAGATGGACGAAGACGACGAAGAACAAGAAAAAAAA
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ري م	141 TCATAGATTACTGCAACAGTTCCCCTGGACTGGAAAAGTTTCTTGCCTGGCTTACAGA 1200 14
3 8	201 AGCTGAAACAACTGCCAATGTCCTA
전	
δy	261 CTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGC 132
qq	
δŏ	ACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCTGGA 138
QQ	1962 196
٥y	1381 AGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAG 144
QQ	1962 196
Οy	1441 TGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTG 150
qq	1962
Q	1501 GAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGGCTACAGCTGAAAGATGATGA 15
g	1962
ΟY	1561 ATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGT 162
qq	1962
Οy	1621 ACATAGGGCCTTCAAGAGGGAATTGAAACTAAAGAACCTGTAATCATGAGTACTCTTGA 168
qq	1963 ACAACTGGCTTTAAAGATCAAAATGAAATGTTATCAA
οy	1681 GACTGTACGAATATTTCTGACAGACAGCCTTTGGAAGGACTAGAAAACTCTACAGGA 1/4
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٥٨	1741 GCCCAGAGAGCTGCCTCCTGAGGAGAGCCCCAGAATGTCACTCGGCTTCTACGAAAGCA	1800
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δŽ	CTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCCCTGACTCCCCC	· 0
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ΟŅ	2041 TCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCAT	2000
qq	CTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTGCGC	9
yo g	2101 TCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACCACAACAACAACAACAACAACAACAACAACAACAAC	15
3 8	161 GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGA	2220
ž E	160 GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTC	2219
2 2	221 AGCATCTCACCTTTCCTTTCCACGTCTCCAGGGTCCCTGGGAAA	2280
ž d	220 AGCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGACCATCTGG	7
Qγ	CCC1	234
qq	CCCTACTATATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCA	233
Oy	2341 AATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATA	
QQ	2340 AAIGACAGAGCTCTACCAGTCTTTAGCTGACTGAATAATGTCAGATTCTCTGAGCTTATA	2.37
Οy	2401 GACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTTTATTCTTTGTTTTTTTT	24.50
qa	2400 GACTGCCATGAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCTG	240
QY	2461	25
QQ	2460 AGCIGCATGIATHICTTICGACCACACCACAAGCAAAATGACCAGCCCATGGA	107
ΟY	, 2521 CCIGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAA	4 0
qq	2520 CCTGCAGATTATTAATTGACCACTATTATGACCGCCTGGAGCAAGAGCAAAA	100
QY	7 2581 TITGGTCAACGTCCTCTCTGCGTGGATAIGTCTCTGAACTGGCTGCTGCAATGTTTATG	A 263
qa	2580 TTTGGTCAACGTCCCTCTCTGCGGTGGATATGTGTCTGAACTGGCTGCTGAATGTGTGTG	, ,
Qy	y 2641 TACGGGACGAACAGGGAGGATCCGTGTCTTGTAAAACTGGCATCATTTCCTTGTT 1	5 - 5 5 - 5 5 - 5
qa	2640 TACGGGACGAACAGGGATCCGTGTCTTTTAAAACTGGCATCATTTCLIG	9 6
ΟY	2701 TAAAGCACATITGGAAGACAAGTACAGATACCTITITCAAGACAAGTGGCAAGTTCAACACAACA	
qa	2700 TAAAGCACATTIGGAAGACAAGTACAGATACCTTITCAAGCAAGTGGCAAGTICAACA	Ñ
QY	2761 A 27	
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PAT 18-JUN-2001
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Shortened dystrophin
Patent: UP 199318467-A 1 24-NOV-1999;
SCIENCE & TECH AGENCY,NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
OS Unidentified
   1215 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 1274
                                      541 TGCTGAGGACACATTGCAAGCACACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 600
                                                                    601 CCAGTITCATACTCATGAGGGGTACATGATTTGACAGCCCATCAGGGCCGGGTTGG 660
                                                                                                                661 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 720
                                                                                                                                                           721 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 780
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Strandedness: Both;
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JP 1999318467-A/1.
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STIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
DN JP 1999318467-A/4
PD 24-NOV-1999
PP 08-MAY-1999 JP 1998142134
PR SINICHI TAKEDA
PC C12N15/09, A61K48/00, C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
FH Key Location/Qualifiers
FT Source /organism='Unidentified',
                                PAT 18-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTCTTCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AGTITIGCCICAACAAGIGAGCATIGAAGCCAICCAGGAAGIGGAAATGIIGCCAAGGCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAAATGCACTATTCTCAACA 300
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0; Mismatches 7; Indels
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/organism="unidentified"
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JP 1999318467-A/4.
                                  Shortened dystrophin.
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                                                                                                                                                                                                                                                                             1095 GAGCTATGCCTACACAGGCTGCTTATGTCACCACCACTGCACCCTACACGGAGCCCATT 1154
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                                                Score 769.2; DB 6;
Pred. No. 8.5e-188;
                                            27.9%; Scor.
96.0%; Pred. No. o..
0; Mismatches
      /db_xref="taxon:32644"
853 c 859 g
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AF339031 3521 bp mRNA linear VRT 20-APR-2001 Danio rerio dystrophin (dmd) mRNA, partial cds, alternatively

AF339031.1 GI:13699249

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DEFINITION ACCESSION VERSION KEYWORDS

AF339031

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ILISMETEERGELERVLNDLEGENRKLQAEYDRLKKAHDHKGLSPLPSPPOMLPVSPQ
SPRDAELIABAKLLRQHKGRLEARMQILEDHNKQLESQLTRLRQLLEGTESKVNGTAL
SSPSTASPRSDTSLASLRVAASQTTETMGDDELSSPTQDASTGLEDVIEQLNNSFPHS
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KVKQMTESMNLAWANTKRAGDKEADLEAGLRQLQHYYLDLEKFLNNLTEAETTANVL
QDATFKEGLLENPATVRHLLEQWQDLQAEIDAHRETYHSLDENGHRIVSSLEGTDNAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="RFCRHWEDSHAKLTARVLTLONMYKDSSDWLEARKRVEPLIKKA
                                                                                                                                                Dystrophin and Dp71, two products of the DMD gene, show a different pattern of expression during embryonic development in zebrafish mech. Dev. 102 (1-2), 239-241 (2001)
                                                                                                                                                                                                                                                                                                                          Submitted (22-JAN-2001) Laboratoire de Physiopathologie Retinienne, EMI 99-18 INSERM-Universite Louis Pasteur, 1, Place de l'Hopital, Strasbourg 67091, France
Location/Qualifiers
                                                                                                           Bolanos-Jimenez, F., Bordais, A., Behra, M., Strahle, U., Sahel, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1038 AICACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGCAAACA 1097
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 TIGAAGATTIAAAAGGCCAAAAIGCAGATGTCAAGCAACTTTCTAAGGATCTACAGCAGT 233
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                                                                                                                                                                                                                                                                              2 (bases 1 to 3521)
Bolanos-Jimenez, F., Rendon, A. and Strahle, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="between 25508 and 25058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAK38376.1"
/db_xref="G1:13699250"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="dystrophin"
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1098 TCTGTAGATGGACAGAAGACGCTGGGTTCTTTACAAGACACTCATAGATTACTGCAAC 1157
                                                    1218 ATGTCCTACAGGATGCTACCCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAG 1277
                                                                                                                            1278 AGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATC 1337
                                                                                                                                                               1338 ACAACCTGGATGAAAACAGCGAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAG 1397
294 ACGACGACACAAAGCAAAGTGAAAATGACCGAGAGCATGAATCTGGCTTGGGCCAACA 353
                                   354 TCAAAAAGCGTGCAGGGGACAAGGAGGCAGATCTGGAAGCTGGACTTCGGCAGTTGCAGC 413
                                                                                                                                                                                                   1398 TCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGT 1457
                                                                                                                                                                                                                                      1458 CTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTT 1517
                                                                                                   1578 CTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGA 1637
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Torpedo californica, cDNA to mRNA.
Torpedo californica
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elssmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
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Draft entry and computer-readable sequence for [Unpublished (1990)]
2178 ACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCCAGCATCTCAGGACTTTC 2237
                  C (bases 1 to 2654)

Ravin, A.J., Dyer, S.M., Yeadon, J.E. and Burden, S.J.
Multiple dystrophin isoforms are associated with the postsynaptic or Torpedo electric organ
J. Physiol. (Paris) 85 (3), 131-133 (1991)
                                                         2238 TITCCACGICIGICCAGGGICCCTGGGAGAGGCCAICICGCCAAACAAAGIGCCCIACT 2297
                                                                             1488 TICATGCGTCTGTTGAAAGCCCTCTCGAACGCTCTATTTCACCCAACAATGTCCCCTACT 1547
                                                                                                                 2298 ATATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACC 2357
                                                                                                                                 2358 AGTCTTTAGGTGACTGAATAATGTCAGATTCTCAGCTTATAGGACTGGCATGAAACTCC 2417
                                                                                                                                                                                            2418 GAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGGATGTGATGCCT 2477
                                                                                                                                                                                                                                                 2478 IGGACCAGCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATT 2537
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Yeadon, J.E., Lin, H., Dyer, S.M. and Burden, S.J.
Dystrophin is a component of the subsynaptic membrane 92064638
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by S.J.Burden, 06-AUG-1990.
Biology Dept, 16-820
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LSQPRSPAQILISLESEERGELERILADLEDENRNLOSSYEKLKQQHDHKGLSPLPSP
PEMMPISPQSRRDAELIABAKLLRQHKGRLEARMQILEDHNKQLESQLHRLRQLLEQP
QAEVRVNGTSVSSPSTSSQRSDSSQPVLLHGVGSQTSGILGEDDLLSAPQSTSSELED
VMEQLSSSFPSSQRRDTPGKKNKEVPM"
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RKYAEEVKVENDKLSNRSVDWQKRIDEALKRLLELQDSMDELNKLKRGAEAIKDTWQP
VGLLIDEALGOHIEKVVKYRAEIAPWRENVTHMNDLASQFTPPDIGLSPYNLNQLEDL
NTRWKLLQVSIDELLKGLHEARRDFGPPSQHPLSTSVGGPWERAISPNKVPYXINHOT
OTTCWDHPKMTELYQSLADLNNVRFSAYRTAWKLRRLQKALCIDLLSLPSACEAFDOH
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SFGGSNIEPSYRSCPQFANNR PEIBAALFLDWMRLEPQSLVMMPVLHRVAAAETAKHQ
AKCNICKECPIIGFRYRSLKHFNYDVCQSCFFSGRTAKGHKMHYPMVEYCTPTTSGED
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                                                                                                                                                                                                                               /translation="SGEQWKRLQISLQDFLTWMNLKNDELRRQMPIGGDAPTVCQQND
                                                                                                                                                                                                                                                                                                                                        NIKQNDQLLDILEJINCLFSIYDRLEQEHSNLVNVPLCVDMCLNWLLNVYDTGRTCKI
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24.8%; Score 685; DB 5; Length 2654;
Best Local Similarity 71.0%; Pred. No. 5.2e-166;
Matches 907; Conservative 0; Mismatches 370; Indels

Conservative 0; Mismatches 370; Indels
                                                 /organism="Torpedo californica"
/db_xref="taxon:7787"
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                                                                                                                                                                                 /product="dystrophin"
/protein_id="AAC38002.1"
/db_xref="G1:397971"
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                   Location/Qualifiers
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Cambridge, MA 02139.
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ROD 27-APR-1993
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Hoffman, E.P., Monaco, A.P., Feener, C.C. and Kunkel, L.M.
Conservation of the Duchenne muscular dystrophy gene in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2625 IGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTAAAACTG 2684
                                                                                                                                                                                                                                                                                                                                                                                                                                     2565 AGCAAGAGACAAATTTGGTCAACGTCCCTCTCTGGGTGGATAIGTGTGTGTGAACTGGC 2624
                                                                                                                                                                                                                                                                                                                                                                                                                  2445 ATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAATG 2504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2505 ACCAGCCCATGGATATCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGG 2564
                                                                                                                                                                                                                                                                                                                                                       2385 GATTOTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGG 2444
                                                                                                                                                                                                                                2265 AGAGGGCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACAACTT 2324
                                                                                                                                                                                                                                                                                            2325 GCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCA 2384
                                                                                                                                                                                                                                                                                                                                                                        2205 ACAGGGACTTTGGTCCAGCAICTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGG 2264
                                                                                                         2145 CCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCC 2204
                                                                                                                                                                                                                                                                                                            2085 TTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACA 2144
                                                                                                                                     661 CACGGIGGAAACICTIGCAGGIGICIATAGAIGAGCTICIGAAGCAGCIGCAIGAGGCIC 720
                                                                          601 TCACACCACCTGATATCCAATTATCCCCGTACAATCTAAACCAGTTGGAGGATCTGAACA 660
linear
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Mouse dystrophin mRNA, partial cds.
M18025
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Mouse adult heart, cDNA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 TICCTICACACCATITGGAAGCICCTGAAGACAAGTCATITGGCAGTICATTGATGGAGA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 GTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540 CTGCTGAGGACACATTGCAAGGACAGAGATTTCTAATGATGTGGAAGTGGTGAAAG 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 ACCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGGCCCATCAGGGCCGGGTTG 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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0; Mismatches 151; Indels
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                                                                                                            /protein_id="AAA37530.1"
/db_xref="GI:192972"
/db_xref="taxon:10090"
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744 bp upstream of PstI site.
                                                       /note="dystrophin"
                                                                                    /codon_start=3
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ROD 23-AUG-1995
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Blake, D.J., Schofield, J.N., Zuelligy, R.A., Gorecki, D.C., Phelps, S.R., Barnard, E.A., Edwards, Y.H. and Davies, K.E. Gutrophin, the autosomal homologue of dystrophin Dpil6, is Proc. Natl. Acad. Sci. U.S.A. 92 (9), 3697-3701 (1995)
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KCCKDIOAEIDHNDIFKSIDGNROKMVKALGNSEEATMLOHRLDDMNORWNDLKAKS
ASIRAHLEASAEKWNRLLASIEELIKWINKDEELKOMPIGGDVPALOLOYDHCKVL
ASIRAHLERSEKERSVLNANDGARVFLADOPIEAPEBPRRUPOSKTELTPEERAGNIAKAMRK
GSSEVREKWENLMAVTSNWQROVGRALEKLRDLGGAMDDLDADMKEVGANGRAWRRVG
DLIIDSLQDHIEKTLAFREEIAPINLKVKTMNDLSSQLSPLDHPSLKMSRQLDDNM
1020 TTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGG 1079
                                                                                                                                                     1080 GAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACGGCTGGGTTCTTTTACAAGACA 1139
                    1140 CTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACAG 1199
                                                                                               Direct Submission
Submitted (15-DEC-1994) D.J. Blake, Institute of Molecular
Medicine: Molecular Genetics, John Radcliffe Hospital, Oxford,
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                                                                                                                                                                                                                                                                                                          1200 AAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGGTAAGGA 1245
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/product-a-G-utrophin (predicted protein)"
/protein_id="CAA58496.1"
/db_xref="GI:793852"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="brain"
/clone_lib="adult mouse brain"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name="G-utrophin"
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/db_xref="SPTREMBL:Q61636"
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/db_xref="taxon:10090"
/clone="AU#3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMGUTRPH
3161 bp
Wormsculus mRNA for G-utrophin.
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G-utrophin.
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Mus musculus
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PUBMED
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AUTHORS
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KEYWORDS
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RWKLLQVSVDDRLKQLQEAHRDFGPSSQHFLSTSVQLPWQRSISHNKVPYYINHQTQT
TCWDHPKMTELGQSLADLNHVRESAYRTAIKIRRLQKALCLDLLELNTTNEVFKQHKL
TCWDHPKMTELGQSLADLNHVRESAYRTAIKIRRLQKALCLDLLELNTTNEVFKQHKL
NQNDQLLSVPDVINCLTTYDGLEQLHKDLVNVPLCVPMCLMVYDTGRTKIRV
NQNDQLLSGYRGLEEKYRCFFERFYNGPFERCOMCLMGLLHDAIQIPQLGEVARF
GSLNIEDSVRSCFQONNNKPEISYREFTONMHLEPGSWYLHYRVARAFTAKHQAK
GNICKECPIYGFRYRSLKHFNYDVCQSCFFSGRTAKGHKLHYPWYBYCJTPTSGEDYR
CNICKECPIYGFRYRSLKHPNYDVCQSCFFSGRTAKGHKLHYPWYBYCJTPTGSEDYR
FHDDTHSTEXAYAFRAQMFTNGSTLPOYGYLEGDNLEFTLISWMPEHYDPSQSPQL
FHDDTHSTEXAYAFRAQMETNGSTLDSSTTGSYBDEHALIQQYCQTLGGESPYS
GORSPADILKSYBREERGELERIIADLEBEQNRLQVEYEQLKEQHLRRGLPPYGSPDS
IVSPHTYSEDSELIAEAKLLRQHKGRLERRNOILEDHNKQLESQLHRLRQLLRGQDSD
SRINGVSWARSPQHALRYSLDFORPORPHQAASEDLLAPPHDTSTDLTDVWEQINST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Gaps
                                                                                                                                                                                                                                                                                                                                                                             21.9%; Score 604.8; DB 10; Length 3161; 63.5%; Pred. No. 3e-145; tive 0; Mismatches 532; Indels 9;
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784 c 802
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Matches 943; Conservative
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PN 3P 1999318467-A/6
PN 3P 1998142134
PR SINICHI TAKED
PC CLONIS,00, A61K48/00, C12N15/00
PC Strandedness: Both;
CC Strandedness: Both;
CC Topology: Linear;
FH Key
FT source 1.3163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear PAT 18-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2656 GAGGAICCGIGICCTGICTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGA 2715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1709 AAAAATTCGGGTACAGAGTCTGAAGATTGATGATGTCTCTCCAAAGGCCTCTTAGA 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                        2596 TCTCTGCGTGGATATGTGTCTGAACTGGCTGCAATGTTTATGATACGGGACGAACAGG 2655
                                                                                                                                                                                                                                                                           2416 CCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGC 2475
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                                                                                                                                                                                                                                                                                          2356 CCAGICITIAGCIGACCIGAATAATGICAGATICICAGCITATAGGACIGCCAIGAAACT 2415
                                                                                                                                                                                                                                       2296 CTATATCAACCACGAGACTCAAACATGCTGGGACCATCCCAAAATGACAGAGCTCTA 2355
                                                                                                                                                                                        2176 GGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGACTTTGGTCCAGCATCTCAGCACTT 2235
                                                                                      2116 TAACCTCAGGACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGTGGCCGTCGA 2175
                                      2476 CTTGGACCAGCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAA
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                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                           2242 CACGTCTGTCCAGGGTCCCTGGGAGAGGCCATCTCGCCAAAAAAGTGCCCTACTATAT 2301
                                                                                                                                                                        2302 CAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTC 2361
                                                                                                                                                                                                               1062 CAACCACGAGACTCAAACATTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTC 1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus dystrophin-related protein 2 B-form splice AF195788.1 GI:11066166
                                                                                  Score 565.6; DB 6; Length 3163;
Pred. No. 4.2e-135;
0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (Dases 1 to 3073)
Roberts, R.G. and Sheng, M. Association of dystrophin-related protein 2 (DRP2) with Postsynaptic densities in rat brain Mol. Cell. Neurosci. 16 (5), 674-685 (2000)
     /organism='Unidentified'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2722 GTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGA 2761
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    .3163
    /organism="unidentified"
    /db_xref="taxon:32644"
    731 c 720 q 782

                                                    720 g
                                                                                 20.5%;
98.4%;
                                                                                             Matches 571; Conservative
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                                                                                         Similarity
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/ Translation="MOPLWOGCPYTLPRCHEWHAADRFHHSSSLRNTCPOPOVRAAV
TIPAPPWDGAGDPCLSPRLMGSVGAVGPLEPSAMNLCWNEIKKKSHNLRPREAFSD
HSGKLOLPLDEIDINLSCNCBELSAOLPLGGDVALVOGEKETHARPEEVKSKGPYTY
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SVLESAQAFLSQHPFEELESSHESSTPTRORGIOLSFEVWKGATVASELWEKLTAR
LEFREBFSPKDGVKLVNDLAHQLAISDVHLSMENSRALED INVERVEVKGATVASELWEKLTAR
LEFREBFSPKDGVKLVNDLAHQLAISDVHLSMENSRALED INVERVEVORT
LARAEREEBERGILVNPLCVDMSLNSTATALEIFNEHDLOASEHWDNVVEVTUC
KEKLOYLESQVANSGSKCDORHLGALLHEATOVPROLGEVAAFGGSNVEPSVRSCFFS
SIKCFRVIGSSENWILSPSCSETPASSPWLHATOVPROLGCTEV
STGKPVIEDSGSTLWVNLLSALHEATOVPROLGEVAAFGGSNVEPSVRSCFFS
SIKCFRVIGSCSTATAKLHYPINTSSENWEDFATILKRFRSKQI
DSLSPDDSIDEDOYLLRHSSPITUREAGOAPCSGAPTILKRFRSKQI
DSLSPDDSIDEDOYLLRHSSPITUREAGOAPCSGAPTILKRFRSKQI
LOGELRRIKWQHEEAVEAPTILAEGSAAATPDHRNBELLAERIILROHRSRLETRWQIL
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AADTALAATALAAGSAAATPDHRAFFSNASSPRULALAASS
2 (bases 1 to 3073)
Roberts, R.G. and Sheng, M.
Direct Submission
Submitted (18-0CT-1999) Division of Medical and Molecular Genetics,
SEI 9RT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="splice acceptor AG dinucleotide used by A-form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="DRP2; membrane-associated cytoskeletal protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contains two spectrin repeats; WW domain; 2Z domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="dystrophin-related protein 2 B-form splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.0%; Score 523.4; DB 10; Length 3073; 62.0%; Pred. No. 3.5e-124; tive 0; Mismatches 506; Indels 0; Gaps
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                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAG28485.1"
/db_xref="G1:11066167"
                                                                                                                                                                                                                                                                      /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 /gene="Drp2"
69. 70
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2683 TGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACGTTTTCAAGCA 2742
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                                                                                                                                                                 2023 TCGAGGAGAAATTGCGGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCA 2082
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                                                      1843 CTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGA 1902
1783 TCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCA 1842
                                                                                                                                      913 GGCAATGGAGGAACTGAGCAGTACTTTGACCCAAGCAGGGAGTCCGAGCCACATGGGA 972
                                                                     1753 AGTGGCCAATTCA 1765
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AF195787 3140 bp mRNA linear ROD 02^{-Ml} Rattus norvegicus dystrophin-related protein 2 A-form splice

DEFINITION RESULT 11 AF195787

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FSKHPORGYLDVOSVLESDCSETPASSPMLPHADTHSRIEHFASRLAEMESONCSFFN
DSLSPDDSIDEDOYLLRHSSPTTOREPAFGQOAPCSMATESKGELEKILAHLEDENNI
LQGERRRLKWQHEEAVEAFTLAEGSAEATPOHRNEELLAAFEARILRQHKSRLETRWQIL
ELOSPLSKLKWQHEEAVEAFTLAEGSAEATPOHRNEELLAAFSRQSSGSPHPREKGQTTPOTE
EDHNKQLESQLORLKELLLQPPTESDGNGSAGSSLASSPRQSEGSHPREKGQTTPOTE
AADDVGSKSQDVSHSLEDIMEKLRHAFPSVRSSDVTANTLLAS"

a 864 c 794 g 690 t 2 others
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SVLESAQAFLSQHPFEELBESTSPRORIOUSRFWURQATVASELWELTAR
SVLESAQAFLSQHPFEELBESTLOAGAGVRATWEPIGDLFIDSLPEHIQAIK
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SLKORVDLGQTCFLTGGRASKGNKLHYPIMEYTPTSSRNMRDFATTLKNKFRSKQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-OCT-1999) Division of Medical and Molecular Genetics, Gurmitted (18-OCT-1999) Division of Medical School, 8th Floor, Guy's Hospital, Guy's Tower, London GKT Medical School, 8th Floor, Guy's Hospital,
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                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /orde="DRP2; membrane-associated cytoskeletal protein; /note="DRP2; contains two spectrin repeats; WW domain; ZZ domain" /codon_start=1
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                                                                                                                                                                                                                                                             Roberts, R.G. and Sheng, M.r. Rated protein 2 (DRP2) with Association of dystrophin rat brain postsynaptic densities in rat brain Mol. Cell. Neurosci. 16 (5), 674-685 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
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variant (Drp2) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Roberts, R.G. and Sheng, M.
Direct Submission
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                                                       AF195787.1 GI:11066164
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                                                                                                              Rattus norvegicus.
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                                               1663 AATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACT 1722
                                                                                              1783 TCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCA 1842
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Human dystrophin-related protein 2 (DRP2) mRNA, complete cds.
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(bases 263 to 3189)

Roberts, R.G., Freeman, T.C., Kendall, E., Vetrie, D.L., Dixon, A.K., Characterization of DRP2, a novel human dystrophin homologue
96225452
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KPV1EASQFLEWVNLEPQSMVMLPVLHRVTIAEQVKHQTKCS1CRQCPIKGFRYRSLK
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ELRRIKWQHEEAAEAPSLADGSTEAATDHRNEELLAEARILRQHKSRLETRWQILEDH
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DVGSKSQDVSLCLEDIMEKLRHAFPSVRSSDVTANTLLAS"
                                                             2683 TGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCA 2742
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/protein_id="AAC50538.1"
/db_xref="GI:1353782"
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/db_xref="taxon:9606"
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/map="Xq22"
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/gene="DRP2"
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                                                        1423 CATGAACTICAAGIGGAGTGAACTICGGAAAAGTCTCTCAACAITAGGICCCAITIGGA 1482
                                                                                                                                      1483 AGCCAGTICTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCT 1542
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                                                                                               552 CATGAATCTGTGGTTGGAATGAAATAAAAAGAAGTCTCACAAACCTCCGCGCTCGCCTAGA 611
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tive 0; Mismatches 506; Indels
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 630)
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Cross, G.S., Speer, A., Rosenthal, A., Forrest, S.M., Smith, T.J.,
Edwards, Y., Filnt, T., Hill, D. and Davies, K.E.
Deletions of fetal and adult muscle cDNA in Duchenne and Becker
muscular dystrophy patients
EMBO J. 6 (11), 3277-3283 (1987)
88111512
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                                                                          2503 TGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCT 2562
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Human fetal mRNA fragment of DMD gene (DMD= Duchenne muscular
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Best Local Similarity 90.18; Pred. No. 4.88-112;
Matches 510; Conservative 0; Mismatches 56; Indels 0
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Duchenne muscular dystrophy
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Human Duchenne muscular dystrophy (DMD) mRNA, complete cds.
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                                                                                                                                                                                                                                                                             1040 CACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATC 1099
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                                                                                                                                                                                                                                     800 AATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGG 859
                                                                                                            860 CTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTT 919
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Homo sapiens brain cDNA to mRNA.
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                                                                                                                                                                                                          HYCQSLNQDSPLSQPRSPAQILISLESEERGELERILADLEEENRNLQAEYDRLKQQH
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PPQDTSTGLEEVMEQLNNSFPSSRGHNVGSLFHMADDLGRAMESLVSVWTDEEGAE"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (29-APR-2002) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Pred. No. 5.3e-107;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 4 Row: j Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5032296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trains lation="MREQLKGHETQTTCWDHPKWTELYOSLADLNNVRFSAVRTAMKL RRLQKALCLDLLSLSAACDALDQHNLKQNDQPWDILQIINCLTTIYDRLEGBHNNLVN VPLCVDWCLNWLLNVYDTGRTGRIRVLSFRTGIISCKAHLEDKYRYLKQYASSTGF CORRLCLLHUSIQIPRQLGBVASFGGSNIEPSYNSCEGFANNFEIEAALFLDWMKLEPDWAAFTAKHQAKONICKECPIIGFRRSLKHPNYDICOSCFFSGRVAKGHKMHYPWVBYCTPTTSGEDVRDFAKVLKNKFRTKRYFAKHPRMGYLPVQTVLE
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                                                                                                                                        Shiraki
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/product="dystrophin (muscular dystrophy, Duchenne and
Becker types)"
                                                                                                                             CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Sh

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

http://www.systemsbiology.org

contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
URL: http://mgc.nci.nih.gov
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1. .4658
                                                              Email: cgapbs-r@mail.nih.gov
                                 help desk
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                                                        Gaps
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Length 4658;
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16.6%; Score 457; DB 9; Le
100.0%; Pred. No. 5.5e-107;
tive 0; Mismatches 0;
                                                      457; Conservative
                               Similarity
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Best Local S
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April 25, 2003, 07:25:57 ; Search time 384:993 Seconds (without alignments) 16150.348 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                      US-09-845-416-9_COPY_540_3300
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Maximum DB seq length: 5000
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain,

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 whether and cysteine-rich domains of dystrophin or utrophin genes. The domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) invention also relates to a recombinant linked to an expression control element. The dystrophin minigene in operable linkage with an expression useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy (BMD) and containing nucleotides 1-1668 (N-terminus, dystrophin minigene delta3849 containing nucleotides 1-1668 (N-terminus, and CR domain) and 11047-11058 (dystrophin last 3 amino acids). rod repeats, H1 and H4 domains and a cysteine rich domain of a Example 1; Page 48-49; 71pp; English.

DB 24; Length 3858; ; 0 0; Indels Sequence 3858 BP; 1189 A; 866 C; 905 G; 898 T; 0 other; 0; Mismatches 100.0%; Score 2761; Pred. No. 100.08; Similarity Query Match Local

61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAACTACTCGATCCTGAAGA 120 1 GCCAGACCTAITIGACTGGAATAGTGTGGTTTGCCAGCAGTCAGCCACACAACGACTGGA 60 Gaps Matches 2761; Conservative g ð

121 TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTCTTCCA 180

GATCACGGTCAGTCTAGCACAGGGATATGAGAGAACTTCTTCCCCTAAGCCTCGATTCAA 360

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540 421 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 480 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC

601 CCAGTITCATACTCATGAGGGGTACATGATTGGACAGCCCCATCAGGGCCGGGTTGG

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g ò 1801 GGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAACCTGCACTCCGCTGACTGGCAGAG 1860 1741 GCCCAGAGAGCTGCCTGAGGAGAGCCCCAGAATGTCACTGGGCTTCTACGAAAGCA 1800 1621 ACATAGGGCCTTCAAGAGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGA 1680 2160 ACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTTGA 2219 1681 GACTGTACGAATATTTCTGACAGACAGCCTTTGGAAGGACTAGAGAAACTCTACCAGGA 1740 1561 ATTAAGCCGGCAGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGT 1620 1501 GAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGGCTACAGCTGAAAGATGATGA 1560 1381 AGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAG 1440 1920 AGGTTCCGATGATGCAGTCCTCTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAG 1979 1321 TCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGA 1380 1081 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACAC 1140 1620 AGATGGGCAAACATCTGTAGATGGACAGAGACCGCTGGGTTCTTTACAAGACAC 1679 1141 TCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACAGA 1200 1201 AGCIGAAACAACIGGCAAIGICCIACAGGAIGCIACCGIAAGGAAAGGCICCIAGAAGA 1260 1021 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG 1080 1440 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAAGGTGCTTCA 1499 1380 GAAAGAGTTGAATGACTGGGTAACAAAAACAGAAAGAAGAACAAGGAAAATGGAGGAAGA 1439 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACATAAGGTGCTTCA 960 841 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGGAAAAATGGAGGAAGA 900 781 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 840 g Qγ Ωÿ qq δŏ qq Qγ pp qq ÓΥ QY q g ó QY g Qγ QQ Óγ g Qγ g op δ ò

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2340 GGCTGAGGACCAATACTGAGTGGGAAAATTGAACCTGCACTCCGCTGACTGGCAGAG 2399
                             1861 AAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 1920
                                       1921 CCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGGGATCTCCT 1980
                                                                                                                                                       2101 TCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCT 2160
                                                                                                                                                                                              2161 GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCC 2220
                                                                                                                                                                                                                                    2700 GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGAAGCCCACAGGGACTTTGGTCC 2759
                                                                                                                                                                                                                                                                         2281 AAACAAAGTGCCCTACTATATCAACCAGGAGACTCAAACAACTTGCTGGGACCATCCCAA 2340
                                                                                                                                                                                                                                                                                                               2341 AATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAG 2400
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                                                                                                                  2041 TCTGAAAGAAGGAGGGAGGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCAT
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AAD37257 standard; DNA; 4825 BP.

RESULT 2 AAD37257

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AAD37257;

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N.terminal or modified N.terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The comprising dysteine rot a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control control element, in a recombinant adeno-associated virus or retrovirus is dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophy (DMD) and Becker muscular vector plasmid construct containing human dystrophy minigenes, a muscle
                                                                                             spectrin;
                                                                                                                                                                                                                                                                                                                                                                                                               New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GATCACGGTCAGTCTAGCACAGGGATATGAGAGAAACTTCTTCCCCTAAGCCTCGATTCAA 360
                                                                          Human; dystrophin minigene; muscular; gene therapy; utrophin; spect; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCCAGACCTATTTGACTGGAATAGTGTGGGTTTGCCAGCAGTCAGCCACACAAAGGACTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4825 BP; 1369 A; 1175 C; 1204 G; 1077 T; 0 other;
                                            Adeno-associated virus vector plasmid, AAV-MCK-delta3849.
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               21-AUG-2002 (first entry)
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Matches 2761; Conservative
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                                                                                                                                           Chimeric - Homo sapiens
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2401 GACIGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTC 2460
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                                                                                                                                                                                               1921 CCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCT 1980
                                                                                                                                                                                                                             1861 AAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 1920
                                                                                                                                                                         ATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGT 1620
                                                                                                       ACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGA 1680
                                                                                                                1681 GACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAGGA 1740
                                                                                                                                             1741 GCCCAGAGAGCTGCCTCCTGAGGAGAGGCCCAGAATGTCACTCGGCTTCTACGAAAGCA 1800
             2677 AGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAG 2736
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3817 CCTGCAGATTATTAATTGTTGACCACTATTATGACCGCCTGGAGCAAGAGCACAACAA 3876
2521 CCTGCAGAITATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAAAA 2580
                             2581 TTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAACTGGCTGAATGTTTATGA 2640
                                     3877 ITTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAACTGCTGCTGAAGTTTATGA 3936
                                                           2641 TACGGGACGAACAGGGAGGATCCGTGTCCTTTTAAAACTGGCATCATTTCCCTGTG 2700
                                                                   1937 TACGGGACGAACAGGAGGAGGATCCGTGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTG 3996
                                                                                        3997 TAAAGCACATTIGGAAGACAAGTACAGATACCTTTICAAGCAAGTGGCAAGTICAAGG 4056
                                                                                                                                                                                                                        Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3849.
                                                                                                                                                                          AAD37263 standard; DNA; 4848 BP.
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.

Chimeric - Cytomegalovirus. Chimeric - Homo sapiens. Chimeric - Unidentified.

WO200183695-A2.

08-NOV-2001.

27-APR-2001; 2001WO-US13677.

28-APR-2000; 2000US-200777P.

(XIAO/) XIAO X.

WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain,

Example 1; Page 68-70; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control control element. The dystrophin minigene in operable linkage with an expression control control element, in a recombinant adeno-associated virus or retrovirus is dystrophy (BMD) in a mammalian subject. The present sequence is AAV ector plasmid construct containing human dystrophin minigenes, a cytomegalovirus (CMV) promoter and a small polya signal sequence.

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61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 120
                                                                                                                                                                      121 TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATGACTCTTCCA 180
                                                                                                                                                                                                                                                                                                                                   241 ACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAAATGCACTATTCTCAACA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1920 CCAGTTTCATACTCATGAGGGTACATGATGGATTTGACAGGCCCATCAGGCCGGGTTGG 1979
                                                                                                                                                                                                                                                                                                                                                                   361 GAGCTATGCCTACACACAGGCTGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATT 420
                                                            0; Gaps
                                                                         1 GCCAGACCTATTTGACTGGAATAGTGTGGTTTGCCAGCAGTCAGCCACACAACGACTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                   421 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 480
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                                                                                                                                                                                                                     181 AGITITGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAATGTTGCCAAGGCC
                                  DB 24; Length 4848;
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                                                           Indels
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                         Query Match 100.0%; Score 2761; Best Local Similarity 100.0%; Pred. No. 0; Matches 2761; Conservative 0; Mismatches
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1981 CATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCC 2040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1861 AAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1801 GGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAACCTGCACTCCGCTGACTGGCAGAG 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1681 GACTGTACGAATATTTCTGACAGGCAGCCTTTGGAAGGACTAGAGAACTCTACCAGGA 1740
                                                                                                                                                                                                                                                                                                    1501 GAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGA 1560
                                                                                                                                                                                                                        AGGTICCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAG 1440
                                                                                                                                                                                                                                TGAACTTCGGAAAAAGTCTCTCTAAACTTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTG 1500
                                                                                                                                                                                       1321 TCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGA 1380
                                                                                                                                                                                               CTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCCAAGGTGAAATTGAAGC 1320
                                                  1081 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACAC 1140
                                                                                    1141 TCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACAGA 1200
                                                                                            2460 TCATAGATTACTGCAACAGTTCCCCTGGACATGGAAAAGTTTCTTGCCTGGCTTACAGA 2519
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                               2641 TACGGGACGAACAGGGAGGATCCGTGTCTTTTAAAACTGGCATCATTTCCCTGTG 2700
                                                                                                                                                                                                                             2461 AGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGACCAGCCCATGGATAT 2520
                                                                                                                                                                                               2521 CCTGCAGATTATTAATTGTTTGACCACTATTATGACCGCCTGGAGCAAGAGCACAACAA 2580
                                                                                                                                  2281 AAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAA 2340
                                                                                                    2341 AATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAG 2400
2161 GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human dystrophin minigene delta3990.
                                                                                                                                                                                                                                                                                                                                                                                                        AAD37234 standard; DNA; 3999 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Becker muscular dystrophy; ds.
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WPI; 2002-049342/06.
 (XIAO/) XIAO X.
    Xiao X;
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a Example 1; Page 46-47; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, The dystrophin minigene operably linked to an expression control control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human hinge HI and rods RI and R2), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

Sequence 3999 BP; 1223 A; 907 C; 933 G; 936 T; 0 other;

0; Indels 141; Gaps Score 2610; DB 24; Length 3999; Pred. No. 0; 0; Mismatches 94.5%; 95.1%; datches 2761; Conservative Similarity Query Match

61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 120 1 GCCAGACCTATTTGACTGGAATAGTGTGGTTTGCCAGCAGTCAGCCACACAACGACTGGA 60 g δ ò g ò

TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTCTTCCA 180 121

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361 GAGCTATGCCTACACACAGGCTGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATT 420

TGAAGTAAACCIGGACCGITAICAAACAGCITTAGAAGAAGTAITAICGIGGCTICTITC 540

TGCTGAGGACACATTGCAAGGACACAAGGAGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 600 541

601 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 660 661 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 720 721 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 780 1021 TGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGG 1080 1081 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGAC-- 1138 1680 GCCTGACCTAGCTCCTGGACTGACCACTATTGGAGCCTCTCCTACTCAGACTGTTACTCT 1739 901 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAAAAAGGTGCTTCA 960 1740 GGTGACACAACCTGTGGTTACTAAGGAAACTGCCATCTCCAAACTAGAAATGCCATCTTC 1799 1139 ------ACTCATAGATTACTGCAACAGTTCCCCTGGACCTGGAAAA 1179 1800 CTTGATGTTGGAGGTACCTACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAA 1859 1180 GTITCITGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCCG 1239 1240 TAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGA 1299 1300 CCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCA 1359 1360 AAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTGGA 1419 2040 AAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGA 2099 1420 TAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTT 1479 1480 GGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTGCAGGAACTTCTGGTGTG 1539 781 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 2100 TAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCAATTT 1139 ---á Db qq δ δy g oγ q ò g δ qq δλ qq ŏ QΩ δ qq ò g a δy g ò g q δ δ δy d pp δλ

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2620 CTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTAA 2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2500 AAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCG 2559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2440 CTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCA 2499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2320 AACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAA 2379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2380 TGTCAGATICTCAGGTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTG 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2260 CTGGGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAAC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2140 GAACACCAGAIGGAAGCIICIGCAGGIGGCCGICGAGGACCGAGICAGGCAGCIGCAIGA 2199
                                                                                                                                                                                                                                                                                                                                                                                                  2080 CCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCT 2139
                                                                                                                                                                                                                                                                                                                                                            2020 ACTICGAGGAGAAATIGCGCCICTGAAAGAGAACGIGAGCCACGICAAIGACCIIGCICG 2079
                                                                                                                                                                                                                                                                                                                      1960 GCAGCCCGTGGGCGATCTCCTCTTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGC 2019
                                                                                                                                                                                                       1780 CACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 1839
                                                                                                                                                                 1660 TGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGCAGCAGCTTTGGAAGG 1719
                                       1600 AGTICAGAAGCAGAACGATGTACATAGGGCCTICAAGAGGGAATIGAAAACTAAAGAACC 1659
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The comprising also relates to a recombinant adeno-associated virus (AAV) invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element. The dystrophin minigene deno-associated virus or retrovirus is control element, in a recombinant adeno-associated virus or retrovirus dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                   Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCCAGACCTATTTGACTGGAATAGTGTGGTTTGCCAGCAGTCAGCCACACAACGACTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 141; Gaps
                                                 94.5%; Score 2610; DB 24; Length 4966; 95.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4966 BP; 1403 A; 1216 C; 1232 G; 1115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                         Adeno-associated virus vector plasmid, AAV-MCK-delta3990.
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                                                                                                                                                 3420 GCAAGTGGCAAGTTCAACAGGA 3441
                                                                                                                               2740 GCAAGTGGCAAGTTCAACAGGA 2761
                                                                                                                                                                                                                                                AAD37256 standard; DNA; 4966 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                   Becker muscular dystrophy; ds.
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Matches 2761; Conservative
                                                                                                                                                                                                                                                                                                                    21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                                     AAD37256;
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TGAAG TGAAG TGAAG TTTCC TTTCC TTTCC TTTCC TTTCAAC TTTCAAC TTTCAAC			1
11111111111111111111111111111111111111	GAGG GAGC GATC GATC GATC GATC SCTT 1111 3CTG 3CTG 1111 1111	NGAAGATGAAG NGAAGATGAAG CTCAGGGTAG CTCAGGGTAG CTCAGGGTAG CTCAGGGTAG AATCAGAAAC ATGAGAAC AAGGTGTTC AAGGTGTTC AAGGTATTGGG AAGGTATTGGG AAGGTATTGGG AAGGTATTGGG AAGGTATTGGG	
14.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.		ATCAGA 	
AGA AGA AGA AAGA AAGA AAGA AAGA AAGA A	CCTCTGACCCT.	CAGGAAATTATCAGAAGAT	
ATTAGGCATAGAGAACT ATTAGGCATAGAGAACT ATTAGGCATCTAATGTACAT IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TCACCACCTCT(TGGAACAGGAAATTATC TGGAACAGGAAAATTATC TGGAACAGGAAAATTATC TGAACAGGAAAATTATC AAATTCAAGATGGAATG HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	
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GCCAG; 	ACAGGCTGCTTA'		
CAACATCGCCAG; 	CACAC.	TACAATTGGGA TACAATTGGGA TACAAGTGGGG TACAAGAGCAG TACAAGAGCAG TACAAGAGCAGG TACAAGAGCAAGG TACTGATTTTT TACTGAGAACAGGAGG TAGTGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	!
CATTCAA LIIIIII ATACCAC ATACCA	CTATGCCTACACA	######################################	
ACATGCA ACATGCAT CTTGAT ACTTAAG ACCTAAAG ACCTAAAG ACCTAAAG GATCACGG	GAGCTATI 	ATATI ATATI CTGAA (1111) CTGAA GCATG (1111) (1111) AGAA TCGAA TCGAA TCGAA	
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io d	CTTGATGTTGGAGGTACCTACTCATAGATTACTGCAACAGTTCCCCCTGGACGACAGTOCTCGAACAGTOCTCGAAAA 261
2617	GTTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGG 12
1240	TAAGGAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGA 129
67	AAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGTGATGATG
1300	ACAGATGTTTATCACAACCTGGATGAAAACAGCCA 135
1360	AGGTTCCGATGAGCAGTCCTGTTACAAAGACGTTTGGA
	GAGTGAACTTCGGAAAAAGTCTCTAAAAACATTAGGTCCATTT 1.
'n	AACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTT 2:
1480	3TGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTG 19
4 1	FGAATTAAGCCGGCAGGCACCTATTGGAGGCGCTTTCCAGC 15
977	TACAGCTGAAAGATGAATTAAGCCGGCAGGCACTATTGGAGGCGACTTTCCAGC 3C
3037	CCTTCAAGAGGGAATTGAAAACTAAAGAACC 16
20	GAGTACTCTTGAGACTGTACGAATATTTCTGACAGGAGCAGCCTTTGGAAGG 17
160	AATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCACCTTTGGAAGG 31
20	ACTCTACCAGGAGCCCACAGAGCTGCCTCCTGAGGAGAGAGGCCCAGAATGT 17
1780 C	CCGCTTCTACGAAAGCAGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 18
40	TCCGCTGACTGGCAGAGAAAATAGATGAGCCCTTGAAAGACTCCAGGAACTTCA 18
277	CTCCCTGACTGGCAGAGAAAAAAAAAAAAAAAAAAAAAA
337	3ATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTG.
1960 G 3397 G	CAGCCCGTGGGGATCTCCTCATTGACTCTCTCCAAGATCACCTGGAGAAAGTCAAGGC 201
2020 A	NGAAATTGCGCCTCTGAAAGAACGTCAGCCACGTCAATGACCTTGCTCG 207
2080 CC	CAGCTTACCACTTTGGGCATTCAGCTCTCACGTATAACCTCAGCACTCTGGAAGACCT

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(XIAO/) XIAO X.
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                                                                                                                                                                                                                                                          AACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCGTTTTCAA 2739
                                                                                                                                                                       CCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAA 2619
                                                                                                                                                                                                        2620 CIGGCIGCIGAAIGITIAIGAIACGGGACGAACAGGGAGGAICCGIGICCIGICITITAA 2679
                                                                                                                                                                                                                                  2260 CTGGGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAAC 2319
                                         3517 CCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCT 3576
                                                                                            AACTIGCIGGGACCAICCCAAAAIGACAGAGCICIACCAGICIIITAGCIGACCIGAAIAA
                2140 GAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGA
                                                 Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3990.
                                                                                                                                                                                                                                                                                 2740 GCAAGTGGCAAGTTCAACAGGA 2761
                                                                                                                                                                                                                                                                                       AAD37262 standard; DNA; 4990 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Cytomegalovirus.
Chimeric - Unidentified.
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is control element, in a recombinant adeno-associated virus or retrovirus dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a cytomegalovirus (CMV) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1861 IGCTGAGGACACATTGCAAGGACACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 TGCTGAGGACACATTGCAAGCACAAAGAAGAATTTCTAATGATGTGGAAGTGGTGAAAGA 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGAAGAGAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GAGCTATGCCTACACACAGGCTGCTTATGTCACCACCTCTGACCCTACAGGGAGCCCATT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AGITITGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAATGTTGCCAAGGCC 240
                                                           New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTTCCT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 141; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 IGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.5%; Score 2610; DB 24; Length 4990; Best Local Similarity 95.1%; Pred. No. 0; Matches 2761; Conservative 0; Mismatches 0; Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4990 BP; 1439 A; 1185 C; 1208 G; 1158 T; 0 other;
                                                                                                                                                                                             Example 1; Page 67-68; 71pp; English.
                                       WPI; 2002-049342/06
                                                                                                                                                             dystrophin gene -
Xiao X;
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3001 GCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGGGACTTTCCAGC 3060
                       1600 AGTICAGAAGCAGAACGAIGTACATAGGGCCTICAAGAGGGAAITGAAAACTAAAGAACC 1659
                                   1660 TGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGGCAGCCTTTGGAAGG 1719
                                                                                1780 CACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 1839
                                                                                                                                                                                                                       1840 GCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCA 1899
                                                                                                                                                                                                                                                         AGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTG 1959
                                                                                                                                                                                                                                                                     1960 GCAGCCCGTGGGGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGC 2019
                                                                                                                                                                                                                                                                                                                  CCAGCITACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCT 2139
                                                                                                                                                                                                                                                                                                                                                                                                            2140 GAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGA 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2200 AGCCCACAGGGACTITGGTCCAGCATCTCAGCACTTTCTTCCACGTCTGTCCAGGGTCC 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2260 CTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGGTCAAAC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTICCIGGGACCATCCCAAAAIGACAGAGCTCTACCAGICTTTAGCIGACCIGAAIAA 2379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2380 TGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTG 2439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3961 AAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTATGACGCG 4020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4021 CCTGGAGCAAGAACAACAATTGGTCAACGTCCCTCTCTGGGTGATATGTGTGAA 4080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2020 ACTICGAGGAGAATIGCGCCTCTGAAAGAGAACGIGAGCCACGTCAAIGACCIIGCTCG
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteinerich domains of dystrophin or utrophin genes. The domains and cysteinerich complexes of dystrophin or utrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control element, the dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is control element, in a mammahinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophin minigene delta4173 containing nucleotides 1-1992 (N-terminus, dystrophin minigene delta4173 containing nucleotides 1-1992 (N-terminus, hinge H1 and rods R1, R2 and R3), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTGGATCCTGAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD: Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 324; Gaps
2680 AACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAA 2739
                  Query Match 87.9%; Score 2427; DB 24; Length 4182; Best Local Similarity 89.5%; Pred. No. 0; Matches 2761; Conservative 0; Mismatches 0; Indels 324:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4182 BP; 1309 A; 927 C; 970 G; 976 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 43-44; 71pp; English.
                                                                                                                                                                                                                                                                                                                               Human dystrophin minigene delta4173.
                                                                                  2740 GCAAGTGGCAAGTTCAACAGGA 2761
                                                                                                                        4201 GCAAGTGGCAAGTTCAACAGGA 4222
                                                                                                                                                                                                                  AAD37230 standard; DNA; 4182 BP
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                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1021 TGATGAATCTAGTGGAGATCACGCAACTGCTGTGGAAGAAGAACAACTTAAGGTATTGGG 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACATAAGGTGCTTCA 960
                                                                                                                                                                                                                             721 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 780
                                                                                                                                                                                                                                                                                                                                                                                                      781 TAGCATGGAAAAAACAAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 840
                                                                                                                                                                                                    601 CCAGTITCATACTCATGAGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 660
                                                                                                                                                                                           421 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 480
                                                                                                                                                         361 GAGCTATGCCTACACACAGGCTGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATT 420
                                                                                                                                                                   181 AGTTTTGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAATGTTGCCAAGGCC 240
                                                            241 ACCTAAAGTGACTAAAGAAGAACATTTCAGTTACATCATCAAGAATGCACTATTCTCAACA 300
                                                                                              GATCACGGTCAGTCTAGCACAGGGATATGAGAGAACTTCTTCCCCTAAGCCTCGATTCAA 360
                                                                                                                                600 ACATGCATTCAACATGGCCAGATATCAATTAGGCATAGAGAAACTACTGGATCCTGAAGA 659
                                                                                                                                                                                                                                                                                                            541 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA
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QQ	198	0 ACTTGAAAAGAGTACAGGACACAGACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGA 11/0
δλ	1177	AAAGTTICTIGCCIGGCTIACAGAAGCIGAAACAACTGCCAATGCTCTACAGGATGCTAC 123
QQ	0	
ΟŊ	123	37 CCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGGGTAAAAGAGCTGATGAAACAATGGCA 1296
QQ	2100	
QY Dp	129	7 AGACCTCCAAGGTGAAATTGAAGCTCACAGAGGTGTTTATCACAACTGGATGAAAACAG 1356
οy	3	7 CCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGAGTCCTGTTACAAAGACGTTT 141
QQ	222	0
Oy Dp	141	47
οy	147	7 TITGGAAGCCAGTICTGACCAGTGGAAGCGTCTGCACTTTCTGCAGGAACTTCTTGCA 1536
qq	2340	TTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGGT 239
9y 0b	1537	GTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGCCACTATTGGAGGCGACTTTCC 159
ζĊ	1597	ACCAGTTCAGAAGCACAAACGATGTAAAATAACACCCGTTTAAAAAAAA
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λ Op Op	1657 2520	ACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGACCAGCCTTTGGA 171.
λy	1717	AGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGAGCTGCCTGAGAGAGA
q	2580	
ζζ	1777	TGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAA 18
ď	64	
<u>ک</u> ۾	1837	CCTGCACTCCGCTGACTGGCAGAGAAATAGATGAGACCCTTGAAAGACTCCAGGAACT 1896
<u>¥</u>	1897	195
ā	2760	TCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGATGATGAGGGATC 281

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2017 GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGC 2076
                                                                                      2077 TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGA 2136
                                                                                                    2940 TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGA 2999
                                                                                                                                               2257 TCCCTGGGAGAGACCATCTCGCCAAACAAGTGCCCTACTATATCAACCACGAGACTCA 2316
                                                                                                                                                                                                             3119
                                                                                                                                                                                                                                      1180 AACAACTIGCIGGGACCAICCCAAAAIGACAGGCICTAACCAGTCTITAGCIGACCTGAA 3239
                                                                                                                                                                                                                                                                                                                  TAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCT 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                              2437 ITGCITGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAA 2496
                                                                                                                                                                                                                                                                                                                                                                          2497 GCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGA 2556
                                                                                                                                                                                                                                                                                                                                                                                                                      2557 CCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTGTGCGTGGATATGTGTCT 2616
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                        Example 1; Page 50-51; 71pp; English.
                                   27-APR-2001; 2001WO-US13677
                                                    28-APR-2000; 2000US-200777P
                                                                                                           WPI; 2002-049342/06
                                                                                                                                                          dystrophin gene -
                                                                       (XIAO/) XIAO X.
WO200183695-A2.
                   08-NOV-2001
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H and H4 domains and cysteinerich domains of dystrophin or utrophin genes. The domerine are a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is control element, in a mammalian subject. The present sequence is human dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene deltaisia containing nucleotides 1-1341 (N-terminus, hinge H1 and rod R1), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids). Sequence 3531 BP; 1071 A; 809 C; 824 G; 827 T; 0 other;

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Ouery Match
Best Local Similarity 88.2%; Pred. No. 0;
Matches 2434; Conservative 0; Mismatches 0; Indels 327;

960 TCCTTCACAGCATTGGAAGCTCCTGAAGACAAGTCATTGGCAGTTCATTGATGGAGGG 1019 241 ACCTAAAGTGACTAAAGAAGAACATTTCAGTTACATCATCAAATGCACTATTCTCAACA 300 301 GATCACGGTCAGTCTAGCACAGGGATATGAGAAACTTCTTCCCCTAAGCCTCGATTCAA 360 GAGCIATGCCIACACACAGGCTGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATT 959 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 480 780 ACCTARAGIGACTARAGAAGAACATTITCAGTTACATCATCAAAIGCACTATTCTCAACA 839 181 AGTITTGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAATGTTGCCAAGGCC 240 61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 120 1 GCCAGACCTATTTGACTGGAATAGTGTGGTTTGCCAGCAGTCAGCCACACACGACTGGA 60 Indels 327; Gaps GAGCTATGCCTACACACACGCTGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATT 361 a g g οy ò

1561 ATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGT 1620 1501 GAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGA 1560 1381 AGGITCCGAIGAIGCAGICCIGITACAAAGACGITIGGAIAACAIGAACIICAAGIGGAG 1440 1441 TGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTG 1500 1653 TGAACTICGGAAAAAGICTCTCAACATTAGGTCCCATITGGAAGCCAGTTCTGACCAGTG 1712 1261 CTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGC 1320 1473 CICCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGC 1532 1321 TCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGA 1380 1201 AGCIGAAACAACIGCCAAIGICCIACAGGAIGCIACCGIAAGGAAAGGCICCIAGAAGA 1260 1021 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG 1080 1081 AGATCGATGGCCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTACAAGACAC 1140 1320 TAGCATGGAAAACAAAGCAATTTACATAGA-----1350 781 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 840 841 GAAAGAGTIGAATGACTGGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAGA 900 901 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 960 721 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 780 601 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCCATCAGGGCCGGGTTGG 660 9 481 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 541 TGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 1351 ------1351 ------1351 ------1351 -----1351 δy ò P oγ ДQ d δy Dβ ŏλ qq δ a δ

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1773 ATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGT 1832
                                 1621 ACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGA 1680
                                               1681 GACTGTACGAATATTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAGGA 1740
                                                                                                                            1741 GCCCAGAGAGCTGCCTCCTGAGGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCA 1800
                                                                                             1801 GGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCGCTGACTGGCAGAG 1860
                                                                                                                                                                                       1861 AAAAATAGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 1920
                                                                                                                                                                                                                                   1921 CCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGGGATCTCCT 1980
                                                                                                                                                                                                                                                                                   2133 CCTCAAGCTGCGCCAAGCTGAGGTCAAGGGATCCTGGCAGCCGGGGGGATCTCT 2192
                                                                                                                                                                                                                                                                                                                    CATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCC 2040
                                                                                                                                                                                                                                                                                                                                2041 TCTGAAAGAAGGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCAT 2100
                                                                                                                                                                                                                                                                                                                                                                                                              TCAGCICTCACCGIATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCT 2160
                                                                                                                                                                                                                                                                                                                                                                                                                              2373 GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCC 2432
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCCACAGGGACTTTGGTCC 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2433 AGCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGACCATCTCGCC 2492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2281 AAACAAAGTGCCCTACTATATCAACCAGGAGACTCAAACAACTTGCTGGGACGATCCCAA 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2341 AATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAG 2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2401 GACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTC 2460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2461 AGCTGCATGTGATGCCTTGGACCAGCAACCTCAAGCAAAATGACCAGCCCATGGATAT 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAGAGGACAAAA 2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2733 CCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAGAGCACAACAA 2792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2581 TTTGGTCAACGTCCCTCTGCGTGGATATGTGTCTGAACTGGCTGAATGTTTATGA 2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2641 TACGGGACGAACAGGGATCCGTGTCTTTTAAAACTGGCATCATTTCCCTGTG 2700
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified domains and domains, rod repeats, utrophin or a spectrin gene, HI and H4 invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control control element. The dystrophin minigene in operable linkage with an expression control control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
2913 TAAAGCACATTIGGAAAACAAGTACAGATACCTTTTCAAGCAAGTGGGAAGTTCAACAGG 2972
                                                                                                                                                                                                                                                                                             Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 327; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCCAGACCTATTTGACTGGAATAGTGTGGGTTTGCCAGCAGTCAGCCACACAAAGGACTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24; Length 4498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4498 BP; 1251 A; 1118 C; 1123 G; 1006 T; 0 other;
                                                                                                                                                                                                                                                             Adeno-associated virus vector plasmid, AAV-MCK-3531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.0%; Score 2097; DB 24;
88.2%; Pred. No. 0;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 62-63; 71pp; English.
                                                                                                                                                            AAD37258 standard; DNA; 4498 BP.
                                                                                                                                                                                                                                                                                                                                   Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                             21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 88.2%
Matches 2434; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                               WO200183695-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (XIAO/) XIAO X.
                                              2761 A 2761
                                                                               2973 A 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2001
                                                                                                                                                                                                 AAD37258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xiao X;
                                                                                                                               RESULT 9
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	241 AC
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3 6	61 GAGCTATGCCTACACACAGG
3 6	21 TCCTTCACA
S &	481 TGAAGTAAACCTGGACCGTTATC
g &	GAAGTAAACCTGGACCGTTATCAAAAAACACTTTATAAAAAAAGAAGTGGTGAAAGA 600 GCTGAGGACACATTGCAAGCAACGAGAGAGAGTTTATAAAAAATGATGTGAAGTGAAAGA 600
qq	ATTICTAATGATGTGGAAGTGGTGAAGA 18
Qy Dh	601 CCAGTITCATACICATGAGGGGTACAIGATGGAITIGACAGCCCATCAGGGCCGGGIIGG 660
δλ	661 TAATATTCTACAATTGG
g S	1957 TAATATTCTACAATTGGGAAGTGGGTAGGTTGGTTGGGGAATGCCTCAGGGTAGGTA
g g	201
οy	781 TAGCATGGAAAACAAAGGAATTTACATAGATTTTAATGGATCTCCAGAATCAGAAACT 840
Q	2077 TAGCATGGAAAAACAAAGCAATTTACATAAGA
ΩŸ	841 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGA
οg	2108 21
Qy	901 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 960
Q	2108 210
Q	961 AGAAGAICTAGAACAAGAACAAGICAGGGICAAITCICICICACICACAGGGGGGGGGG
ΩD	2108 210
Qy	1021 TGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGG 10
qq	2108
Qy	1081 AGATCGATGGGCAAACATCTG
q	2108
ò	1141 TCATAGATTACTGCAACAGTTCCCCTGGACCTGGAAAGTTTCTTGCCTGCC

qq			~
Qy	1201 AGCT	CIGAAACAACIGCCAAIGICCIACAGGAIGCTACCGGAAGGAAAGGCICCTAGAAGA 1260 	0 6
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QQ	O١	ACACAGATGTTTATCACAACCTGGATGAAAACAACCAAAAAAAA	c
δy	38	AGGTTCCGATGATGCAGTCCTGTTACAAGACGTTTGGATAACATGAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT	. 6
QQ :		SGTTCCGATGATGCAGTCCTG41ACAGATGCCCATTTGGAAGCCAGTTCTGACCAGTG 1500	0
ž ž		ASSECTATE CONTROLL	6.0
δλ	Ĺ,	01 GAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGA 1560	29
qa A	2470 G	AAGCGTCTGCACCTTTCLTTSCACCTTTCAGCAGTTCAGAAGCAGAACGATGT 1620	50
i d	5		68
Qy	1621 A	CATAGGGCCTTCAAGAGGGAATTGAAACTAAAGAACCTGTAATCATGAGTACTCTTGA 1680	80
qq	Ω	CATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAUTACLILIIGA 2017 CATAGGGCCTTCAAGAGGGGAATTGAAAACTAAAGAACCTGTAATCATGAUTACLILIGA 2017	, 0
QY	φ w	ACTGTACGAATATTCTGACAGAGCAGCCTTTGGAAGGACTRGAGAAACICLACCAGAATATTCTGACAGGAGCTTTGGAAGGAAGGAAACICLACCAGGA 1773 	60
δy		CCCAGAGAGCTGCCTCCTGAGAGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCA 1800	00
qq	2710	0 0	9 0
QY	1801	82	329
qq	2770	92	320
ΟŊ	1861	AAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGCCACGGATGAGCTGGGAACTGGAAAGAGCCACGGATGAGCTGGAAAGAGAGAG	989
qq	2830	AAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGALGAGCTGGGAAGTTGAAGATAGATGAGACCCTTGAAAAGACTGCAGGAACTTCAAGAGGCCACGGATGAGATGAGATGAGATGAGAAGATGAGAAGATGAGAAGA) (
ΟY	1921	CCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCT 198	980 949
ДQ	2890	CCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCTTGGCAGCCCGTGGGGGGGG	040
Oy	1981	CATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAAAAAAAA	500
qq	2950	CATTGACTCTCTCTCTCTCCAAGATCACCICGAAGAAAAAAAAAA	100
Qy	2041	30	90
g	3010	21	
QY	2101	31	12
qq	3070	22	C)
QY	2161	31	-
QQ	.,	22	C
QY	• •	32	C)
QO		•	1

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2281 AAACAAAGTGCCCTACTATTCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAA 2340
            2341 AATGACAGACTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAG 2400
                                                  2461 AGCTGCATGTGATGCCTTGGACCAGCAAACCTCAAGCAAAATGACCAGCCCATGGATAT 2520
                                                                                                                                  2521 CCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGGAAGAGCACAAAA 2580
                                                                                                                                                                          Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                        2581 TITGGTCAACGTCCCTCTGCGTGGATATGTGTCTGAACTGGCTGCTGAATGTTTATGA 2640
                                                                                                                                                                                                                   3550 TTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAACTGGCTGCTGAATGTTTATGA 3609
                                                                                                                                                                                                                                                 2641 TACGGGACGAACAGGGAGGATCCGTGTCCTTTTAAAACTGGCATCATTTCCCTGTG 2700
                                                                                                                                                                                                                                                             3610 TACGGGACGAACAGGAGGAGGATCCGTGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTG 3669
                                                                                                                                                                                                                                                                                         New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human dystrophin minigene delta3510.
                                                                                                                                                                                                                                                                                                                                                                                                     AAD37240 standard; DNA; 3510 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Becker muscular dystrophy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-049342/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dystrophin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200183695-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N·terminal or modified N·terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control control element, in a recombinant adeno-associated virus or retrovirus is dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene deltasio containing nucleotides 1-1668 (N·terminus, Hinge H1 and rods R1 and R2), 8407-10227 (rods R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                     61 ACAIGCAITCAACAICGCCAGAIAICAATTAGGCATAGAGAAACIACTCGAICCIGAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                   600 ACAIGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTCTTCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AGTITTGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAATGTTGCCAAGGCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAAATGCACTATTCTCAACA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GATCACGGTCAGTCTAGCACAGGGATATGAGAGAACTTCTTCCCCTAAGCCTCGATTCAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels 348; Gaps
                                                                                                                                                                                                                                                                                                                                     1 GCCAGACCTATTTGACTGGGAATAGTGTGGGTTTGCCAGCAGTCAGCCACAACGACTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GAGCIATGCCTACACACAGGCTGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 TCCTTCACAGCATTIGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGAGGAGAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 TGAAGTAAACCIGGACCGTTATCAAACAGCTTTAGAAGAAGIATTATCGIGGCTTCTTTC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 IGCTGAGGACACATIGCAAGCACAAAGAAGATITCTAATGATGTGGAAGTGGTGAAAGA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.4%; Score 2055; DB 24; Length 3510; 87.4%; Pred. No. 0; Live 0; Mismatches 0; Indels 348;
                                                                                                                                                                                                                                          Sequence 3510 BP; 1073 A; 787 C; 828 G; 822 T; 0 other;
Example 1; Page 51-52; 71pp; English.
                                                                                                                                                                                                                                                                                                        Matches 2413; Conservative
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                            Query Match
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	781 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 	GGATCTCCAGAATCAGAAACT 840 	
		AACAAGGAAAATGGAGGAAGA 900 	
		ACAACAACATAAGGTGCTTCA 960 	
	1440 961	CACTCACATGGTGGTGGTAGT 1020 	
. ~ .	1021	AAGAACAACTTAAGGTATTGGG 1080 	
o 5-	1081	3GTGGGTTCTTTACAAGACAC 1140	
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× 4	1677		
<u> ></u>	1201 AGCTGAAACAACTGC	126	
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q	1677	16	
λ	1321 TCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAG	167	
g	1677	9 5	
27	1381 AGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAACA	167	
ą	1677	1 1	
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QY	1681	AGGACTAGAGAACTCTACCAGGA 1740	
QΩ	1872	180	
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                                                                                                                                      2101 TCAGCTCTCACCGTATAACCTCAGCACTCTGAAGACCTGAACACCAGATGGAAGCTTCT 2160
1921 CCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCT 1980
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
Adeno-associated virus vector plasmid, AAV-MCK-3510.
                          Becker muscular dystrophy; ds.
                                                                                               28-APR-2000; 2000US-200777P.
                                                                                   27-APR-2001; 2001WO-US13677.
                                            Chimeric - Unidentified.
                                      Chimeric - Homo sapiens
                                                                                                                                     WPI; 2002-049342/06.
                                                          WO200183695-A2.
                                                                                                            (XIAO/) XIAO X.
                                                                      08-NOV-2001.
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a

Example 1; Page 63-65; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control control element, in a recombinant adeno-associated virus or retrovirus is dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophy (DMD) and Becker muscular vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.

Sequence 4476 BP; 1252 A; 1096 C; 1127 G; 1001 T; 0 other;

1356 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAACTACTGCATCCTGAAGA 1415 61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 120 121 TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTCTTCCA 180 181 AGTTTTGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAATGTTGCCAAGGCC 240 241 ACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAATGCACTATTCTCAACA 300 Indels 348; Gaps 1 GCCAGACCTATTTGACTGGAATAGTGTGGTTTGCCAGCAGTCAGCCACACAACGACTGGA 60 301 GATCACGGTCAGTCTAGCACAGGGATATGAGAGAACTTCTTCCCCTAAGCCTCGATTCAA 360 74.4%; Score 2055; DB 24; Length 4476; 87.4%; Pred. No. 0; 0; 0; Mismatches Best_Local Similarity 87.49 Matches 2413; Conservative Query Match g ò δ q qq ò ð g ò ą

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361 GAGCTATGCCTACACACAGGCTGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATT 420
                                                 421 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 480
                                                                                                    481 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 540
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                                                                                               1621 ACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGA 1680
                                                                     2448 GAAGCGICIGCACCITICICICCAGGAACTICIGGIGGCIACAGCIGAAAGAIGAIGA 2507
      .-----CAGTTCTGACCAGTG 2447
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene in operable linkage with an expression control element. The draft in a recombinant adeno-associated virus or retrovirus is control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin in DNA fragment encoding rods R22, R23 and R24, hinge H4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                           2641 TACGGGACGAACAGGAAGGATCCGTGTCTTTTAAAACTGGCATCATTTCCCTGTG 2700
                                                                                                          3468 CCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAA 3527
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human dystrophin rod, hinge and CR domain regions encoding DNA \sharp 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.8%; Score 1623; DB 24; Length 2169; 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                   AAD37232 standard; DNA; 2169 BP.
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                1139 ACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACA 1198
                                                  1199 GAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGTAAGGAAAGGCTCCTAGAA 1258
                                                                                   1259 GACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAA 1318
                                                                                                                     1319 GCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTG 1378
                                                                                                                                                       1379 GAAGGTTCCGATGATGCAGTCCTGTTACAAGACGTTTGGATAACATGAACTTCAAGTGG 1438
                                                                                                                                                                                        1439 AGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAG 1498
                                                                                                                                                                                                                          1499 TGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGGCTACAGCTGAAAGATGAT 1558
                                                                                                                                                                                                                                                           1559 GAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGAT 1618
                                                           1619 GTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTT 1678
                                                                                                                                                                                                                                                                                                                             1679 GAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAG 1738
                                                                                                                                                                GAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAG 1798
                          CAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCGGTGACTGGCAG 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                  1859 AGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTG 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1919 GACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTC 1978
        0; Gaps
                                                                                                                                                                                                                                                                                                     1979 CTCATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCG 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2039 CCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGC 2098
                                                                                                                                                                                                                                                                                                                                                                        2099 ATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTT 2158
                                                                                                                                                                                                                                                                                                                                                                                                          2159 CTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGT 2218
                                                                                                                                                                                                                                                                                                                                                                                                                                            1022 CTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGT 1081
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    0; Mismatches
Matches 1623; Conservative
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1082 CCAGCATCTCAGCATTTCTTTCCACGTTCCAGGGTCCCTGGGAGAGAGCCATCTCG 1141
                                                         2339 AAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTAT 2398
                                                                                                                                   2459 TCAGCTGCATGTGATGCCTTGGACCAGCACACCTCAAGCAAAATGACCAGCCCATGGAT 2518
                                                                                                                                                                                              2519 ATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAAC 2578
                                                                                                                                                                                                                                                                                                                 2579 AATTIGGTCAACGICCCTCTGTGCGTGGATATGTGTCTGAACTGGCTGCTGAATGTTTAT 2638
                                                                                                                                                                                                                                                                                                                                                                            2639 GATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTTAAAACTGGCATCATTTCCCTG 2698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     2399 AGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus vector plasmid, AAV-MCK-3447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD37260 standard; DNA; 4414 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Homo sapiens.
Chimeric - Unidentified.
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control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence. The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression of the dystrophin minigene in operable linkage with an expression of the dystrophin minigene in operable linkage with an expression of the dystrophin minigene with the dystrosmin of the dystrophin minigene with the dystrophin discussion the dystrophin minigene with the dystrophin discussion discuss New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a Example 1; Page 65-66; 71pp; English. dystrophin gene

Sequence 4414 BP; 1255 A; 1075 C; 1086 G; 998 T; 0 other;

1957 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 2016 1777 IGAAGIAAACCIGGACCGITAICAAACAGCITIAGAAGAAGIAITAICGIGGCIICIIIC 1836 099 1537 ACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAAATGCACTATTCTCAACA 1596 TAATATICTACAATIGGGAAGTAAGCTGATIGGAACAGGAAAATTAICAGAAGAIGAAGA 720 009 421 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 480 481 IGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTC 540 rgrigataccaccrarccagaraagaagrccarcrraargracarcarcarcrcrrcra 1476 GAGCIATGCCTACACACAGGCTGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATT 420 AGTTTTGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAATGTTGCCAAGGCC 240 241 ACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAAATGCACTATTCTCAACA 300 301 GATCACGGTCAGTCTAGCACAGGGATATGAGAAACTTCTTCCCCTAAGCCTCGATTCAA 360 121 TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTCTTCCA 180 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTGCATCCTGAAGA 120 0; Mismatches 185; Indels 411; Gaps 1 GCCAGACCTATTTGACTGGAATAGTGTGTGTTTGCCAGCAGTCAGCCACACAAGGACTGGA 60 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCCATCAGGGCCGGGTTGG 541 TGCTGAGGACACATTGCAAGGACAGAGAGATTTCTAATGATGTGGGAAGTGGTGAAAGA DB 24; Length 4414; Best Local Similarity 78.4%; Score 1623; Matches 2165; Conservative 601 661 361 1417 61 1357 181 셤 ò q ŏ g ŏ q ò qq ŏ δ g ò g ô g οy ò ŏ

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1681 GACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAACTCTACCAGGA 1740 1741 GCCCAGAGGTGCCTCCTGAGGAGAGAGCCCAGAATGTCACTGGGCTTCTACGAAAGCA 1800 1561 ATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGT 1620 1621 ACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGA 1680 1441 TGAACTICGGAAAAAGTCTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTG 1500 1501 GAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGGCTACAGCTGAAAGATGATGA 1560 1381 AGGTICCGAIGAIGCAGICCIGTIACAAAGACGITIGGAIAACAIGAACITCAAGIGGAG 1440 1201 AGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGTAAGGAAAGGCTCCTAGAAGA 1260 1261 CTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGC 1320 2542 ICAAAATGAAATGITATCAAGTCITCAAAAACTGGCCGITTTAAAAGCGGATCTAGAAAA 2601 1321 TCACACAGATGTTTAICACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGA 1380 2602 GABABAGCARTCCATGGGCAAACTGTATTCACTCAAACAAGATCTTCTTTCAACACTGAA 2661 2662 GAATAAGTCAGTGACCCAGAAGAAGGAAGCATGGCTGGATAACTTTGCCCGGTGTTGGGA 2721 1141 TCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACAGA 1200 2437 CCTTCTCAAAIGGCAACGICTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 2496 1081 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACAC 1140 2077 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 2136 2137 GAAAGAGTTGAATGACTGGGTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAGA 2196 901 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 960 841 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAAAAAGAAGAAAATGGAGGAAGA 900 2497 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTA-------AAGA TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 721 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 2722 TAATTTAGTCCAAAACTTGAAAAGAGT-----2750 ------2750 -----781 qq δ g QΥ g δλ рp qq δ Ωp δy οq δy a ŏ Ωp QY g δλ ô qq δλ Ω g οy qq pp pp

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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                       Human dystrophin minigene delta3447
                                                                                                  Becker muscular dystrophy; ds.
                                                                                                                                                                                                          28-APR-2000; 2000US-200777P.
                                                                                                                                                                                     27-APR-2001; 2001WO-US13677
                                 21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                           WPI; 2002-049342/06.
                                                                                                                                                                                                                                (XIAO/) XIAO X.
                                                                                                                                           WO200183695-A2
                                                                                                                       Homo sapiens.
                                                                                                                                                                08-NOV-2001.
               AAD37242;
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1801 GGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCGCTGACTGGCAGAG 1860
                                         1861 AAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 1920
                                                     1921 CCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCT 1980
                                                                                                                              1981 CATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCC 2040
                                                                                                                                          2041 TCTGAAAGAGGAGGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCAT 2100
                                                                                                                                                                                                                                                            2161 GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCCACAGGGACTTTGGTCC 2220
                                                                                                                                                                                                      2985
                                                                                                                                                                                                                                                 3045
                                                                                                                                                                                                                                                                        2221 AGCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGCCATCTCGCC 2280
                                                                                                                                                                                                                                                                                                                   AAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAA 2340
                                                                                                                                                                                                                                                                                                                                                             AATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAG 2400
                                                                                                                                                                                                                                                                                                                                                                                                         GACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTTGGATCTCTTGAGCCTGTC 2460
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2461 AGCTGCATGTGATGCCTTGGACCAGCAACCTCAAGCAAAATGACCAGCCCATGGATAT 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2521 CCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAA 2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2641 TACGGGACGAACAGGATCCGTGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTG 2700
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                                                                                                                                                                                     2926 TCTGAAAGAGAGAGGTGAGCGCACGTCAACGTCGCCAGCTTACCACTTTGGCGTTT
                                                                                                                                                                                                                   TCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCT
                                                                                                                                                                                                                              2581 TITGGTCAACGICCCTCTGCGTGGATAIGIGTCTGAACTGGCTGAATGTTTAIGA
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified domains, rod repeats, utrophin or a spectrin gene, H1 and H4 invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control control element. The dystrophin minigene in operable linkage with an expression social for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject The present sequence is human dystrophin minigene delta347 containing nucleotides 1-1992 (N-terminus, finge H1 and rods R1, R2 and R3), 8749-10227 (rod R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, HI and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ACAIGCATICAACAICGCCAGAIAICAAITAGGCATAGAGAAACIACIGGAICCIGAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTCTTCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGTITTGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAATGTTGCCAAGGCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAAATGCACTATTCTCAACA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 185; Indels 412; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCCAGACCTATTTGACTGGAATAGTGTGGTTTGCCAGCAGTCAGCCACACAACGACTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 1611; DB 24; Length 3446; 78.4%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3446 BP; 1074 A; 766 C; 787 G; 819 T; 0 other;
                                                                                                                                   Example 1; Page 53-54; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 2164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                       dystrophin gene -
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AAD37242 standard; DNA; 3446 BP.

ESULT 14 AD37242

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ξ, q	301 G	ATCACGGTCAGTCTAGCACAGGGATATGAGAGAACTTCTTCCCCTAAGCCTCGATTCAA 30
λ Q	61 G 	AGC A
ž d	21 T 	CCTTCAC
yo da	81 20	GAAG AAG
, y 4	41	GCTGAGGACACATTGCAAGC/
ko a	01	CAG
γο 4	61	AATATTCTACAATTGGGA
3 73 2	21 2	ACTGAAGTACAAGAGCAGATGAATCT
3 6 8	81	ATGGAAAAACAAAGCAAT
3 & 2	41	AAAGAGTTGAATGACTGGCTAACAAAAACAGA
5 6 E	39	ATCTT
3 6 5	, io a	GAAGATCTAGAACAAGA
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o v	08	GATCGATGGCAAACATCTGTAGATGGACAGAAGA
oy Oy	1619	GGATGGGCAAACATCIGIAGATGGACAGAAAGATTCTTGCCTGGCTTACAGA 120 AGATTACTGCAACAGTTCCCCTGGACAAAGTTTCTTGCCTGGCTTACAGA 120
qq	1679	TTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTTCAGA 173
Oy Db	1201	AGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGGTAAGGAAAGGCTCCTAGAAGA 1286
Óγ	1261	ATGAAACAATGGCAAGACTCCAAGGTGAAATTGAAGC 13
qq	1784	TCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTAAAAAGCGGATCTAGAAAAA 104
Q dd	1321	TCACACAGATGTTTATCACAACCTGGATGAAAAGACCTGAGATGTCCTGAGATCCTGGATGA 150 TCACACAGAAACTGTATTCAACTGTATTCACTCAAACAAGATCTTCTTTCAACAGA 190 GAAAAAGCAATCCATGGGGAAACTGTATTCACTCAAACAAGATCTTCTTTCAACACTGAA 190
δy	3	AGGTTCCGATG

qq	1904	96
00	1441	ACATTAGGTCC
g qq	1964	 AACT
Οy	1501 (A 156
qq	1999	199
QY	1561	GT 162
Dp	1999	1998
δy	1621	GA 168
QQ	1999	6
QY	1681	74
qq	1999	- 199
QY	1741	A 180
qq	1999	
Oy	1801	186
qq	1999	199
ΟŊ	1861	GACCCITGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 192
QQ	1999	CTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 204
Qy	92	CTCAAGCTGCGCCAAGCTGAG
QQ	2048	GCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGGCCGTGGGCGATGCTGGCTG
δλ	8	CGAGAAAGTCAAGGCACTTCGAGGAAAAAAAAAAAAAAA
QQ	2108	STCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGGGGGGG
QY	2041	CTGAAAGAGAACGTGAGCGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCA 210
Dβ	2168	TGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACIIIGGGCAI 222
Oy	10	TCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCT 2150 10.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.
qq	22	TCAGCITCICACCETAIAACCITCAGCAGCACCACCACCAGCAGGAGGACTTTGGTTC
δλ	16	GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCAGGAAGCCCCACAGGGACTTTGGTTTTTTTT
qo i	90 0	GCAGGTGGCCGTCGACGACGGACCGGACACTCGCGGCGGGGGTCCCTGGGGAGAGAGCCATCTGGC
QY	7 (AGCATULICATION CONTROLL CONTROL CO
g G	7 1	AGCALCLCAGCACTTCCTTCCTTCCTTCCTCTCAAACAACAACTTGCTGGGACCATCCC
Qy da	2281	AAACAAAGIGCCCTACTATATCAACCACACACACATTIIIIIIIIII
2 0	34	AATGACAGAGCTCTACCAGTC
ad	46	
QY	240]	SCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTC 246
qa	2528	CICITGAGCCTGIC 258
Qy	246	1 AGCTGCATGTGTGCGTTGGACCACACACACAAAGCAAAATGACCAGCCCATGCATAT 2520

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2588 AGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGACCAGGCCCATGGATAT 2647
                        2521 CCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAA 2580
                                     2581 ITTGGTCAACGTCCCTCTGCGTGGATATGTGTCTGAACTGGGTGCTGAATGTTTATGA 2640
                                                                                                                         2641 TACGGGACGAACAGGGAGGATCCGTGTCTTTTAAAACTGGCATCATTGCCTGTG 2700
                                                                                       2768 TACGGGACGAACAGGGAGGATCCGTGTCTTTTAAAACTGGCATCATTCCCTGTG 2827
                                                                                                                                                                                       2828 TAAAGCACATTIGGAAGACAAGTACAGATACCTTITCAAGCAAGTGGGAAGTTCAAGG 2887
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AA248567 standard; cDNA to mRNA; 4402 BP. 31-MAR-2000 (first entry) AAZ48567;

A rod shortened dystrophin (deltaDysAx11) encoding nucleotide sequence. Muscular dystrophy; rod domain; adeno-associated virus; AAV; dystrophin gene; truncated; ds.

Homo sapiens.

JP11318467-A.

24-NOV-1999.

98JP-0142134. 08-MAY-1998;

08-MAY-1998;

(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO. (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

98JP-0142134.

WPI; 2000-100771/09.

P-PSDB; AAY59238

gene encoding a shortened dystrophin - useful for the treatment of muscular dystrophy

Claim 7; Page 16-17; 44pp; Japanese.

having at least one rod repeat structure of hinge 1, hinge 4 and rod and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin immune reaction. The present sequence represents a rod shortened yestrophin The invention provides a gene for the treatment of muscular dystrophy

Sequence 4402 BP; 1329 A; 1000 C; 1019 G; 1054 T; 0 other;

0; Indels 735; Gaps h Similarity 73.4%; Score 1281; DB 21; Length 4402; 26; Conservative 0; Mismatches 0; Indels 735; Best Local Similarity /3.4* Matches 2026; Conservative Query Match

1 GCCAGACCTATTTGACTGGGAATAGTGTGGGTTTGCCAGCAGGCACACAACAACGACTGGA 60 à

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61 ACATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGA 120
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                                              121 TGTTGATACCACCTATCCAGATAAGAAGTCCATCTTAATGTACATCACATCACTCTTCCA 180
                                                                                           241 ACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAAATGCACTATTCTCAACA 300
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g	1805	AGGAGGICAAIACIGAGIGGGGGGGGGGGGGGGGGGG
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oy G	1921 C	CTCAAGCTGGGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT
ογ	1981	TCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCC 204
q	1980 C	3CC 203
QY	2041 T	CTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCAT 2100
ΩD	2040 I	CIGAAAGAGAACGTGAGGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCAT 203
οy	2101 T	CAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAACTTC1 210
QO	2100	CAGCTCTCACCGTATAACCTCACCTCTGGAAGACCTGAACACCAGAAACAACAAAAAAAA
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qq	2160	CAGCTGCATGAAGCCCACAGGGACTIIGGICC 221

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GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description BC009242 Homo sapi BI729851 60349511 BI730168 60349711 AL121550 DKF2P/62L AL556247 AL556247 BQ640063 he23904.y
SUMMARIES	BC009242 BI730168 BI730168 AL121550 AL556247 BQ640063
% Query Match Jenath nn	31.7 1490 11 31.7 1490 11 17.9 750 13 17.6 579 9 A 16.2 620 14
Score	874.6 605.4 495.2 486.6 457 446
Result No.	6 5 5 4 5 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

BG719710 602690430 BM488464 pgm2n.pk0 BM659984 BB629984 AK013510 Mus muscu BB610411 BB610411 BB66688 BB666688 A196693 u153e10.y AA460476 ze61e10.r AL641565 A1641ec	BE182065 601804 604 AL796733 AL796733 AL672616 AL672616 BE334408 ug97q06.y BJ036515 BJ036615 BI546771 603191346 BM488542 Pgm2n.pk0 AL795562 AL795552 BJ075057 BL075057	BC011062 Mus muscu BC112445 RST32032 BE201973 f103h06.x B1250598 602993659 AL602076 DKEZp313B B1553820 603190772 B1446561 de24a10.y BF963618 QV2-NN004 BQ304046 QV2-BT0663 BF144271 601796605	AA771140 vt18bb5.r BF22633 uz4dg06.y AW467977 he29908.x B198828 4012-24 M BB677285 BB627285 B1289102 UI-R-DK0- BG207912 RS727400 BE557463 f103h06.y AK020881 Mus muscu BF387048 UI-R-CAI-	
12 BG7 12 13 BM4 12 10 BB6 15 11 AK0 14 10 BB6 14 19 BB6 14 9 AI196 15 1196 16 1196 17 1196 18 12 BB6 18 12 BB6 18 12 BB6 18 18 BB6 18	633 9 AL7965 638 9 AL672616 532 10 BE34408 532 13 BJ036615 541 13 BJ46771 548 13 BM488542 597 9 AL795652 646 13 AL652755 2334 11 BC011062	12 BG21: 10 BE20] 13 B1255 9 AL602C 13 B1553 13 B1545 12 BF963 14 BQ304 12 BF963 13 AP7771	12 BF226 10 AW467 10 AW467 113 B12893 12 BG207 11 AES57 11 BF3870	ALIGNMENTS
435.4 15.8 424.2 15.4 112.8 15.0 412.8 15.0 1 411.2 14.9 1 399.4 14.8 381.8 13.8 345.6 12.6 345.8 12.5	17 345 12.5 18 330 12.0 20 325.6 11.8 21 315.6 11.8 22 310 11.2 24 297.8 10.8 25 276.6 10.0 26 271.6 9.8 2	255.0 254 9.2 250 9.1 230.4 8.3 226 8.2 206.4 7.5 199.2 7.2	184.8 6.7 182.4 6.6 178.2 6.5 173 6.3 175 6.2 156.8 5.7 153.4 5.6 153.2 5.5	RESULT 1 BC009242 LOCUS 42 BC009242

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Greene, Mark Ketteman and Anuradha Madan
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                                                                                                                                                                                    358 t
                                                                                                                                                                                                                     pred. No. 3.36
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NIH-MGC http://mgc.ncl.nih.gov/.
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721 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapDs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
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/clone_lib="NIH_MGC_94"

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1268 GGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACA 1327
                                                                                                   1328 GATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCTGGGAAGGTTCC 1387
                                                                                                                                                                                                            1388 GATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTT 1447
                            1448 CGGAAAAAGTCTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAGCGT 1507
                                                                                                                                                                                                                                                                                                                                                                                                                      1508 CTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGC 1567
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                                                                                                                                     1568 CGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGG 1627
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:10090" /clone="IMAGE:5357187"

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/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3:3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library.
                                                                                                                                                                        1060 AGAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCG 1119
                                                                                                                                                                                                                       1120 CTGGGTTCTTTTACAAGACACTCATAGATTACTGCAACAGTTCCCCCTGGACGTGGAAAA 1179
                                                                                                                                                                                                                                                                        1180 GITICITGCCTGG-CTTACAGAAGCTGAAAC--AACTGCCAATGTCCTACAGATGCTAC 1236
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DKFZp762L078_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
DKFZp762L078 5', mRNA sequence.
                                                                                                                                   DB 13; Length 750;
                                                                                            1 others
                                                                                                                                                          93; Indels
                                                                                                                           17.9%; Score 495.2; DB 13;
85.5%; Pred. No. 2.3e-110;
Live 0; Mismatches 93;
                                                                                        178 g
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                                                                                   BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1596 CAGCAGTICAGAAGCAGAAGGATGTACATAGGGCCTICAAGAGGGAATTGAAAACTAAAG 1655
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                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone (DKFZp762L078) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin. Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 GCCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTT 190
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                                                                                                                        Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="DKEZp762L078"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
                                                                                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                    EST (Ottenwaelder, et al.)
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                                                                                                                                                                                                      Contact: Ottenwaelder B
AL121550
AL121550.1 GI:5927551
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                                                                  Homo sapiens
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/db_xref="txtof">
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/dlone txtof in a Not1-oligo(dr) primer. Five prime end was primed with a Not1-oligo(dr) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA wises of the pCMVSPORT 6 cloned into the Not I and ECO RV sites of the pCMVSPORT 6 cloned into the Not I and ECO RV sites of the pCMVSPORT 6 cloned into the Not I and ECO RV sites of the pCMVSPORT 6 cloned into the Not I and ECO RV sites of the pCMVSPORT 6 cloned into the Not I and ECO RV sites of the pCMVSPORT 6 cloned into the Not I and ECO RV sites of the pCMVSPORT 6 cloned into the Not I and ECO RV sites of the pCMVSPORT 6 cloned into the Not I and 20850, USA Fax: (1) 301 610 8371 EDM in filangelifetech.com URL:

Email: filangelifetech.com URL:

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ptxp://ulllength.invitrogen.com"
                                                                                                                           AL556247 Tr_NFLO06_PL2 Homo saplens cDNA clone CSODKOO1YB17 5 Prime, mRNA sequence.
AL556241 LTI_NFLO06_PL2 Homo saplens cDNA clone CSODKOO1YB17 5 AL556247
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 757)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2305 CCACGAGACTCAAACATGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 2364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: segref@genoscope.ons.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.6%; Score 457; DB 9; Lv
100.0%; Pred. No. 5.3e-101;
ative 0; Mismatches 0;
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BP 191 91006 EVRY cedex - France
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1776 ATGTCACTCGGCTTCTACGAAAGCAGGCT 1804
                      /db_xref="taxon:9606"
                                                                                                                                                                                                                             AL556247.1 GI:12898746
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Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of human retina for the NEIBank splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), (2002) In press
                                                                                                                                                                                                                                              EST 15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // note = "Organ: Eye; Vector: pSPORTI; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORTI vector (Life Technologies) was constructed at the protocols of the SuperScript plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Human Retina cDNA (Un-normalized, unamplified
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                             BQ640063

BQ640063

Homo sapiens cDNA (Un-normalized, unamplified): hd/he BQ640063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strand synthesis was carried out using a Not i primer-adapter [5'-pGACTAGATCTAGATCGCGAGCGCCCCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intranural Sequencing Center (NISC)."
2665 IGICCIGICITITAAAACIGGCAICAITICCCIGIGIAAAGCACAITIGGAAGACAAGIA 2724
                     Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Section on Molecular Structure and Function
                                                                              2725 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGA 2761
                                                                                                  Bethesda, MD 20892-2740, USA
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Seq primer: M13Rp1 reverse primer (ABI).
Location/Qualifiers
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/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: graeme@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="he23g04"
                                                                                                                                                                                                                                                                                                           BQ640063.1 GI:21764522
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301 402 3452
Fax: 301 496 0078
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2316 AAACAACTIGCIGGGACCAICCCAAAAIGACAGAGCICIACCAGICITIAGCIGACCIGA 2375

0; Gaps

Length 620; 0; Indels

Query Match 16.2%; Score 446; DB 14; Best Local Similarity 100.0%; Pred. No. 2.5e-98; Matches 446; Conservative 0; Mismatches 0;

2376 ATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCC 2435

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BG719710
602690430F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4822807 5',
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NHF-WGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and plero Carnicci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                    2436 TTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCA 2495
                                                                                                             2496 AGGAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATG 2555
                                                                                                                                                                                       2556 ACCGCCTGGAGCAAGAGCACAACATTTGGTCAACGTCCCTCTCTGGGTGGATATGTGTC 2615
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                                                      2676 ITAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTT 2735
61 ATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCC 120
                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/lab_host="DH10B"
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Location/Qualifiers
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pgm2n.pk007.117 Normalized Chicken Breast Muscle, Leg Muscle, and pgm2n.pk007.117 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk007.117 5' similar to spiP11533|DMD_CHICK Dystrophin pli1502041 dystrophin, muscle - chicken emb|CAA31746.11 (X13369) dystrophin (AA 1 - 3660) [Gallus gallus], mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 663)
Cogburn,L.A. and Monsonego-Ornan,E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
                                                                                                                                                                                                                                                                                                                                                                                                                             2603 GTGGATATGTGTCTGAACTGGCTGAATGTTTATGATACGGGACGAACAGGGAGGATC 2662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2663 CGIGICCIGICITITAAAACTGGCAICAITICCCIGIGIAAAGCACAITIGGAAGAAAG 2722
                                                                                                                                                                                                                                                                                   2485 GCACAA--CCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATAATTGTTTG 2542
                                                                                                                                                                                                                                                                                                                                                       2543 ACCACTATITATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGC 2602
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                                                                                                                                          AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGGAAGACT 2424
                                                                                                                                                                                                                                                                                                        510 CGTGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAG
                                                                    2305 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 2364
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                                                                                                                                                                                                                                210 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.8%; Score 435.4; DB 12; Length 770; Best Local Similarity 98.3%; Pred. No. 1.1e-95; Matches 451; Conservative 0; Mismatches 6; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cogburn@udel.edu, www.chickest.udel.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2723 TACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGA 2761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
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BM488464
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EST 31-AUG-2001
                                                                                                                                           /note="Vector: pcMvSpORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.38; juvenile muscle 33.38; and epiphyseal growth plate 33.38 of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                 /dev_stage="Breast.leg:Embryo(d19):post-hatch(ld,1,3,5,7,9
/l1 weeks):growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coll EMDH10B"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)" /sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1879 TGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGC 1938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1699 GACAGAGCAGCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCC 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1759 TGAGGAGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATAC 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1819 TGAGTGGGAAAAATTGAACCTGCACTCGCTGACTGGCAGAGAAAATAGATGAGACCCT 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1639 GGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCT 1698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1339 CAACCTGGATGAAAACAGCCAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGATGTGTT 1398
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                                                   /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
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                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                         DB 13; Length 663;
                                                                                                                                                                                                                                                                                                                         15.4%; Score 424.2; DB 13; Length 78.1%; Pred. No. 5.6e-93; tive 0; Mismatches 144; Indels
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

ACCESSION VERSION KEYWORDS

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T (bases 1 to 652)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiranoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Soqabe,Y., Sucuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y., Tanaka,T., Toya,T.,
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I.; Kiyosawa,H.; Kondo,S.; Saito,T.; Shinagawa,A.; Aizawa
Ishii,Y. and Hayashizaki,Y.
Mapphing of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Punc. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIREN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. .. 10 (11), 175-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Mramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primed with a primer [5, GAGAGAGAGACCAACAGGACCTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, adult female
musculus cDNA clone 9930028B14 5', mRNA sequence.
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/db_xref="taxon:10090"
/clone="9930028B14"
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/lab_host="DH10B"
                                                                                     BB629984.1 GI:15399733
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Fax: 81-45-503-9216
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FEATURES

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK013510 . 2135 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900010C03:dystrophin, muscular dystrophy,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                     15.0%; Score 412.8; DB 10; Length 652; 94.1%; Pred. No. 3.4e-90;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                                                                                                                         0; Mismatches
                                                                                                                   148 g
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HTC; CAP trapper.
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AK013510
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Mus musculus
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VPLCVDMCLNWLLNVYDTGRTGRIRVLSFKTGIISLGKAHLEDKYRYLFKQVASSTGF
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457 c 438 g 677 t
                                                                                                                                                                                                                                                                                                                                                                /tissue_type="hippocampus"
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1. 2135
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2665 TGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 2724
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Pred. No. 5e-90;
0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="data source:MGD, source key:MGI:94909,
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/db_xref="MGD:NGI:1905833"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
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/db_xref="GI:12850900"
                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                   /strain="C57BL/6J
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ilarity 94.1%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Arakawa,T., Hara,A., Fukunishi,Y., Karosawa,H., Kondo,S., Yamanaka,I., Saizawa,M., Nishi,K., Kiyosawa,H., Komdo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bano,H., Kasukawa,T., Saito,R., Radto,T., Casterland,T., Gissi,C., King,B., Kochiwa,H., Fleischman,M., Gasterland,T., Cissi,C., King,B., Kochiwa,H., Ruehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Wagner,I., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Bake,J., Boffeeli,D., Bolunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fultita,M., Gariboldi,M., Gutsincich,S., Hill,D., Hofman,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Nordone,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Stocch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Tayashi,R., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' KGAGAGAGARAGACTCTTTTTTTTTTTTTTTTTTY 3'], CDNA was prepared by using trebalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second
                                                                                                                                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishiner, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwaqi, K., Yoneda, Y., Ishikawa, T., Ozawa, Y., Izawa, M., Ohara, E., Watahiki, M., Oneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inouce, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
                                         Genome Res. 10 (10), 1617-1630 (2000)
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SOURCE

COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 704)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Kouda Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

Contact: Yoshihide Hayashizaki, Y. Contact: Yoshihide Hayashizaki
                                                                                                                                                    EST 26-OCT-2001
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-reségac.riken.go.jp,
URL:http://genome.gac.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected connas to prepare full:length cDNa libraries for rapid discovery of new wagi.K., Fuliwake.S., 10 (10), 1617-1630 (2000)
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura Hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-che Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
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/dev_stage="10 day old"
/dev_stage="10 day old"
/note="vector: psPoRT1; Site_1: SalI; Site_2: NotI; This
/note="vector: psPoRT1; Site_1: SalI; Site_2: NotI; This
embryo cDNA libraries (including preimplantation stage
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5 embryos
, and E12.5 female mesonephros/gonad) and one newborn
                                                                                                 BB610411
BB610411 RIKEN full-length enriched, 10 day old male pancreas Mus
musculus cDNA clone 1810074E05 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RIKEN full-length enriched, 10 day old male
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/clone="1810074E05"
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BB610411.1 GI:16451938
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RESULT 11
BB610411
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FEATURES

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ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dr source libraries are cloned unidirectionally with Oligo(dr expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, unselected transcripts from extreambryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the x chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
N., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB66688 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330026B12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                          2305 CCACGAGACTCAAACATGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2365 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2425 GCAGAAGGCCCTTTGGTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA 2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2485 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 2544
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                                                                                                                                                                                                                                                                                                                                                                                                 2605 GGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 2664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.9%; Score 411.2; DB 10; Length 704; 93.9%; Pred. No. 8.7e-90; Live 0; Mismatches 28; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format referencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) ronno, H., Pukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Y. and Hayashizaki, Y. computer based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                    Email: genome-reseggs.riken.go.jp,
URL:http://genome-gsg.riken.go.jp/
URL:http://genome-gsc.riken.go.jp/
URL:http://genome-gsc.riken.go.jp/
URL:http://genome-gsc.riken.go.jp/
URL:http://genome-gsc.riken.go.jp/
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramatsu,Eselected cDNAs to
Normalization and subtraction of cap-trapper-selected cDNAs to
Normalization and subtraction of cap-trapper.selected cDNAs to
Normalization and Hayashi, T. Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Matahiki,M., Voneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                   Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The 1-7.22 Suchiro-cho Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RIKEN full-length enriched, 2 days pregnant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2305 CCACGAGACTCAAACATGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 2364
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
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94.2%; Pred. No. 2.3e-89;
tive 0; Mismatches 26
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E330026B12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425; Conservative
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1 (bases 1 to 854)
Marran, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Martan, M., Hillier, L., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Tan, F., Underwood, K., Moore, B., Tan, F., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ui53alo.yl Sugano mouse liver mia mus musculus cDNA clone
Image:1886154 5' similar to 9b:M18533 DYSTROPHIN (HUMAN); 9b:M68859
Mouse dystrophin mRNA, exons 1-7 and complete cds (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 14-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                2665 TGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTGGAAGACAAGTA 2724
                                                                                                                                                  2485 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 2544
                                                                                                                                                                                                                          2545 CACTATTTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTGCGT 2604
                                                                                                                                                                                                                                                                                                                                                                                            2365 AGCTGACTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 2424
                                                                                                                                                                      Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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314 286 1810
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FEATURES
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/Note="Organ: liver; Vector: pME185-FL3; Site_1: DraIII (CACCATGTGG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer.
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME186-FL3 vector (5' site CACGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the CDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 423)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.-Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie Y., Waterston,R. and Wilson,R.

Unpublished (1997)
                                                                                                                                                                                                                                             sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2365 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA460476 423 bp mRNA linear EST 09-JUN-1 zx61e10.rl Soares_total_fetus_Nb2HF8_9w Homo sapiens CDNA clone IMAGE:795978 5' similar to gb:M18533 DYSTROPHIN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      2305 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2425 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA 2484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2545 CACTATTATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTCTGGGT 2604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 CCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTGGACC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 GGATATGTGTCTCAACTGGCTTCTCAATGTTTATGATACGGGACGAACAGGGAAGATCCG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 AGCTGACCTGAATAATGTCAGGTTCTCCGCGTATAGGACTGCCATGAAGCTCAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 854;
                                                                                                                                                                                                                                                                                                3 others
                                                                                                                                                                                                                                                                                                                                                                                                        31; Indels
                                                                                                                                                                                                                                                                                                                                                          14.3%; Score 395.4; DB 9 93.0%; Pred. No. 6.9e-86; Live 0; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2724 ACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGG 2760
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Double-stranded cDNA was ligated to ECC RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and ECC RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL641565 XGC-neurula Silurana tropicalis cDNA clone TNeu012d20 5', AL641565 AAL641565.1 GI:16793690
          Mashington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
721: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2485 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 2544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.8%; Score 381.8; DB 9; Length 423; 99.2%; Pred. No. 1.2e-82; Live 0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                          /clone_lib="Scares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2664 GTGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTG 2700
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/db_xref="GDB:6039697"
                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                         /clone="IMAGE:795978"
                                                                                                                                                                                           Location/Qualifiers
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394; Conservative
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western clawed frog.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.

Xenopodinae; Silurana.

I (bases 1 to 684)

Sanger Xenopus tropicalis EST project 2001 (10_2001)

L Upublished (2001)

Contact: Huckle E

Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001

TROPICALIS_SEQUENCE_ID: TNeu012d20.sp6
Sequence in From a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

L Coatland/Oualifiers

L GARALON/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="Thwe012200"
/clone=lib="xxCo-neurula"
/dev_stage="neurula"
/dev_stage="neurula"
/dab_bost="scherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI at the 5' end and NotI at the 3' end."
a 175 c 172 g 169 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.6%; Score 346.6; DB 9; Length 684; Similarity 84.9%; Pred. No. 5.8e-74; B8; Conservative 0; Mismatches 69; Indels 0.
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Sequence 193, App
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Sequence 10,
                                                                 April 25, 2003, 08:10:12 ; Search time 62.8837 Seconds
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Sequence 76,
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compuger 1+d
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US-09-244-796-17
US-09-014-969-14
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US-08-139-937-12
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US-08-376-843-38
US-09-434-408-3
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US-08-425-069-3
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Maximum Match 100%
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Sequence 13, App
Sequence 189, App
Sequence 187, App
                                                                                             Sequence 3, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 11, Appli
                                                                                                                                                       Sequence 13, Appl
Sequence 184, App
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                                                                                                                                                                                                      Sequence 370,
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                                                                                 Seguence
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APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTON: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
                       US-08-857-076-44
US-08-61-697-189
US-09-461-697-187
US-09-61-697-185
US-09-671-950-1
US-09-671-950-3
US-09-671-950-5
US-09-671-950-9
                                                                                                                                    US-09-671-950-11
US-09-671-950-13
US-09-461-697-184
US-09-014-583-1
US-09-014-583-1
US-08-961-527-370
                                                                                                                                                                                                              US-08-642-807A-27
                                                                                                                                                                                                                                                                                                                                                                                                                         3: Curtis, Morris & Safford, P.C.
530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Frommer, william S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION 1424
PRIOR APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08257073
Patent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  22277
2499
7174
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1047
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COMPUTER READABLE FORM:
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 linear
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TOPOLOGY:
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APPLICANT: Lewis Randolph V.
APPLICANT: Lewis Michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: ISOLATED DNA OFFICE BOTOLING THE ISOLATED DNA, AND PRODUCTS THEREOF
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                       888 AAATGGAGGAAGAGCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAC 947
                                                                               2153 AAGAAGAAGAAGAAGAAGAAGAAGAAATAGTACCAGAAAATTTGACAACTGA 2210
                                                                                                                                                                                                                                                   948 ATAAGGIGCTICAAGAAGAICTAGAACAAGAACAAGICAGGGICAAITCICICACICA 1005
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44.0%; Pred. No. 0.19;
itive 0; Mismatches 209; Indels 0;
Query Match
Best Local Similarity 51.7%; Pred. No. 0.056;
Matches 92; Conservative 0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPPRATIS: SYSTEM: PC-DOS/MS-DOS
SOFTWATE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OFTWARE: PACEULA...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
APPLICATION AUMBER: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08425069
Patent No. 5728810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 144
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1995 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4
Query Match
Best Local Similarity 44.0
Matches 164; Conservative
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LOCATION: 1..1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
TITLE OF INVENTION: 62
CORRESPONDENCES: 62
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1778 GTCACTCGGGTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAAC 1837
                                                                                                                                                                                                                                                                                                                     1718 GGACTAGAGAAACTCTACCAGGAGCCCAGAGGTGCCTCCTGAGGAGAGAGCCCAGAAT 1777
                                                                                                                                                               1658 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA 1717
                                                                                                                                                                                                                                                                                                                                                                                                 851 GACCTGGAGGATATGGCCCTGGACAACAAGGACCCGGAGGATATGGACCAGGACAACAAG 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           911 GACCATCTGGAGGAGGAGGAGGAGCAGCAGCAGCAGGACCTGGACAACAAGAT 970
1598 GCAGTTCAGAAGCAAAGGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAA 1657
                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/317,844B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5989894th Washington Street CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMBER: US/08/317,844B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinman, Michael B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703) 241-1300
(703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 241-2848
TELEEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1958 TGGCAGCCCGTGG 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1091 AAGGACCAGGAGG 1103
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APPLICANT: Lewis, Ra
APPLICANT: Xu, Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH:
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US-08-317-844B-3
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1598 GCAGTICAGAAGCAGAACGAIGIACAIAGGGCCTICAAGAGGGAAIIGAAAACIAAAGAA 1657
                                                                                                                                                                                                                                                             1658 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA 1717
                                                                                                                                                                                                                                                                                                                               1778 GICACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAAC 1837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          971 TAGGAGGTTATGGACCAGGACAACAAGGTCCAGGAGGATATGGACCAGGACAACAAGGTC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1898 CAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCC 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1031 cagaaganangaaccaggnagracatcracagcagcagcagcagcagcagaccragacaac 1090
                                                                                                                 Y Match 1.4%; Score 38.6; DB 2; Length 1995; Local Similarity 44.0%; Pred. No. 0.19; hes 164; Conservative 0; Mismatches 209; Indels 0; Gaps
                                                                                                                                                                                                                          731 GCAGTGCAGCTGCAGCAGCAGCAGCACCTGGACAACAAGAACCGGGAGGATATGGAC 790
                                                                                                                                                                                                                                                                                             701 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 AAAAAGTTAGACGAAGATAATGCTAAACTTGTTGAGGTTGTTGAAACCACAAGTTTGGAA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            761 IGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATG 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     881 ACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTA 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%; Score 38.2; DB 6; Length 1131;
45.9%; Pred. No. 0.17;
tive 0; Mismatches 153; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gomi, Hideyuki: Hozumi, Tatsunobu: Hattori, Shizuo; Tagawa, Chiaki; Kishimoto, Fumitaka; Bjorck, Lars TITLE OF INVENTION: PROTEIN H CAPABLE OF BINDING TO IGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/376,641
FILING DATE: 07-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 130, Conservative
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                                                                      1..1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
IMMEDIATE SOURCE:
                                                    NAME/KEY: CDS
LOCATION: 1..1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Patent No. 5180810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1131
                                                                                  US-08-317-844B-3
                                                                                                                                                          Matches 164;
                CLONE:
                                                                                                                       Query Match
                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5180810-3
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701 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   761 IGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    821 GATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAAACAGAAGAAGA 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604 GAAAATCAAGGAAAGCTCGAAAATTGGAGCTTGACTATCTCAAAAAATAGATCACGAG 663
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1.4%; Score 38.2; DB 6; Length 1784;
Best Local Similarity 45.9%; Pred. No. 0.23;
Matches 130; Conservative 0; Mismatches 153; Indels 0;
                                                                                                                                                                                          APPLICANT: Gomi, Hideyuki: Hozumi, Tatsunobu; Hattori, Shizuo; Tagawa, Chiaki; Kishimoto, Fumitaka; Bjorck, Lars
TITLE OF INVENTION: PROTEIN H CAPABLE OF BINDING TO IGG
                            397 TTAGAACGTAAATACCAACGAGAAGTAGAAAAACGTTATCAAG 439
941 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAG 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              941 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAG 983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 76, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT APPLICATION NUMBER: 06/09/4,121
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/09/16
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/099,273
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/376,641
FILING DATE: 07-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patent.pm
SEQ ID NO 76
                                                                                                                                         5180810-2
;Patent No. 5180810
                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 1784
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NAME/KEY: CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 ATTAATGGGTGAAAATCAAGATCTTCGAAAAAGAGAGGGACAATATCAGGACAAAATAGA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                874 AGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACG 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1087 AAAAACAATITAAAATTICAAATITTAAAATIGCIGCACCATAAGAIGAATAAAGAGC 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               694 AACAGGAAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATTCCTAAA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 AGCGTGGAACTGGCCTAAAGAATATAACGCGTTACTTAAGGAAAATGAGGAGCTCAAGGT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 AGAACGTGAAAATATCTATCTTATGCTGACGATAAAGAAAAAGATCCTCAATCTAGAGC 380
                                                                                                                                                                                                                                                                                                                                                                              789 AAAAACAAAAGCAATITACATAGAGTTTTAATGGAICICCAGAATCAGAAACTGAAAGGAGT 848
                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **APPLICANT: LINDAHL, GUNNAR; FRITHZ, ELISABET; HEDEN, LARS-OLOF
TITLE OF INVENTION: PROTEIN ARP, WITH IMMUNOGLOBULIN A
TITLE OF INVENTION: PROTEIN ARP, WITH IMMUNOGLOBULIN A
BINDING ACTIVITY, THE CORRESPONDING VECTORS AND HOSTS, REAGENT
KIT AND PHARMACEUTICAL COMPOSITION
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
PFILING DATE: 14-NOV-1988
PRICR APPLICATION NUMBER: 186,097
FILING DATE: 25-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849 TGAATGACTGGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%; Score 38; DB 4; Length 1394; 59.1%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            934 CCAAGTACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACA 981
                                                                                                                                                                                                                                                                                                                                             45; Indels
                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                            NAME/KEY: sig_peptide
LOCATION: 46.87
LOCATION: 46.87
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LTLLGLSLILAGL/IV
                                                                                                                                                                                                                                                                                                                           Best Local Similarity 59.1
Matches 65; Conservative
                                                                                                                                                               NAME/KEY: polyA_signal LOCATION: 1363..1368
                                                                                                                                                                                                                            NAME/KEY: polyA_site
LOCATION: 1382..1394
LOCATION: 46..675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:1:
LENGTH: 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Patent No. 5210183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 131;
                                                                                                                                                                                                                                                                    US-09-247-155-76
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810 GAGTITIAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAA 869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          630 TGGATTTGACAGCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 TGGCTTTGGATAAACATATGATGCATGTAACAATTAGTTATCCCCTACCTGACAATCAGC 408
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48.0%; Pred. No. 0.74;
tive 0; Mismatches 144; Indels 2
                                                          APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                           E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     870 CAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGA 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587 CAATGAGCATTAIGTCAAAATTTCATTAATTGGCTCAGGCA 627
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA (genomic) (p14c15)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGERT INFORMATION:
NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 35,547
REFERENCE/POCKET NUMBER: 28341/33996
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/887,534A
                                                                                                                                                                                                                          STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 22, Application US/08887534A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEX: (312) 474-6408
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 1845 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 135; Conservative
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LOCATION: 856..1842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                       Patent No. 6455323
GENERAL INFORMATION:
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STREET: 200
-mv. Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                    90909
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                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 RNRARSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    882 CAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTAC 941
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## Patent No. 625858
| Patent No. 625858
| GENERAL INFORMATION:
| APPLICANT: SZOSTAK, Jack W. |
| APPLICANT: ROBERTS, Richard W. |
| APPLICANT: ROBERTS, Richard W. |
| APPLICANT: ROBERTS, RICHARD W. |
| TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FORSIONS |
| TITLE OF INVENTION: FUSIONS |
| FILE REFERENCE: 00786/350003 |
| CURRENT APPLICATION NUMBER: US/09/007,005B |
| EARLIER FILING DATE: 1998-01-17 |
| EARLIER FILING DATE: 1997-01-27 |
| EARLIER FILING DATE: 1997-11-06 |
| NUMBER OF SEQ ID NOS: 33 |
| SEQ ID NO 17 |
| LENGTH: 289 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09244796

Fatent No. 6281344

GENERAL INFORMATION:
APPLICANT: SCOSTAK, Jack W.
APPLICANT: ROBERTS, TRICHARD W.
APPLICANT: BOBERTS, TRICHARD W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: FELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PASSESE FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 36.2; DB 4; Length 289; 6.1%; Pred. No. 0.26; tive 99; Mismatches 118; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     942 AACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRCRARGRCRUGGRCR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 6.1%;
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LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     882 CAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTAC 941
                                                                                                                                                                                                                                         0; Gaps
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1.3%; Score 36.2; DB 4; Length 289;
Best Local Similarity 6.1%; Pred. No. 0.26;
Matches 14; Conservative 99; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             942 AACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                        OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/014,969
                                                                                                              ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09014969
Patent No. 5965397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617) 498-8284
(617) 876-5851
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS:
                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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US-09-014-969-14
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APPLICANT:
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                                        FEATURE:
                                                                            FEATURE:
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APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: RAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: DOLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  784 CATGGAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAA 843
                                                                                                                                                                                                                                    724 IGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGCTAG 783
                                                                                                                                                        664 TATICTACAATIGGGAAGTAAGCIGATIGGAACAGGAAAATTAICAGAAGAIGAAGAAC 723
                                                                                                                        0; Gaps
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                                                                                1.3%; Score 36.2; DB 2; Length 2447;
46.8%; Pred. No. 1.2;
tive 1; Mismatches 124; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/630,915A FILING DATE: 03.4PR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: Pennie & Edmonds LLP
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 193, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORREY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,87
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-8864/974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                            0.0ery Match
Best Local Similarity 46.8%
Matches 110; Conservative
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double
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                  ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-014-969-14
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STRANDEDNESS:
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                                                                893 GAGGAAGACCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAAAAG 952
                                                                                                                                                      Gaps
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1.3%; Score 36; DB 4; Length 2873; 52.7%; Pred. No. 1.6; tive 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     856 CTGGCTAACAAAACAGAAGAAGAACAAGGAAAA 890
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                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Plant Metal Transporters FILE REFERENCE: BB1303 US NA CURRENT APPLICATION NUMBER: US/09/461,474 CURRENT FILING DATE: 1999-12-14 EARLIER APPLICATION NUMBER: 60/112,562 EARLIER FILING DATE: 1998-12-16 NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE
                                                                                                                                                                                                          953 GTGCTTCAAGAAGATCTAGAACAAGAAC 980
                                                                                                                                                                                                                                            162 ACACAAGAAAATTCAAGAAGAGGAAC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08139937 Patent No. 5821070
                                                                                                                                                                                                                                                                                                                         ; Sequence 13, Application US/09461474
; Patent No. 6278042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Triticum aestivum
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          0.0ery Match 1.3°
Best Local Similarity 52.7°
Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Allen, Steve
APPLICANT: Rafalski, Ant
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US-09-461-474-13
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LENGIH: 790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  864 CAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAAAGGCCTCTTGGACCTGATCTTGAAG 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924 ACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAAGAG 983
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GENERAL INFORMATION:
APPLICANT: BOARD OF REGENTS OF THE UNIVERSITY OF TEXAS SYSTEM
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3%; Score 35.6; DB 1; Length 4868;
51.9%; Pred. No. 3;
tive 0; Mismatches 74; Indels 0;
  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2041 TGAAAGAAAATCAAGCACTGCCATGGAGATGCT 2074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
                                                                                                                                                                                                                                           P-CJ 9370
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,937
FILING DATE: 20-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: FP-CJ 9790
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 12:
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/979,156
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JMBER: PCT/US93/11310
19-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       NAME: CAMPBELL, CATHEYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEPHONE: 619-535-9001
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH : 4868 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: CDNA
US-08-139-937-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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PCT-US93-11310-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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April 25, 2003, 17:39:49 ; Search time 183.448 Seconds	(without alignments)	16376.941 Million cell updates/sec

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core:	sednence:	Scoring table: IDENTITY_NUC Gapop 10.0	

709820 seqs, 544064369 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

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2: 'Cgn2_6/ptodata/1/pubpna/US06_WW_DUB.seq:*
3: 'Cgn2_6/ptodata/1/pubpna/US06_WW_DUB.seq:*
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5: 'Cgn2_6/ptodata/1/pubpna/US07_NEW_DUB.seq:*
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7: 'Cgn2_6/ptodata/1/pubpna/US08_WW_DUB.seq:*
7: 'Cgn2_6/ptodata/1/pubpna/US08_WW_DUB.seq:*
7: 'Cgn2_6/ptodata/1/pubpna/US09_WW_DUB.seq:*
10: 'Cgn2_6/ptodata/1/pubpna/US09_WW_DUB.seq:*
11: 'Cgn2_6/ptodata/1/pubpna/US09_WW_DUB.seq:*
12: 'Cgn2_6/ptodata/1/pubpna/US09_WW_DUB.seq:*
13: 'Cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: 'Cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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14: 'Cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: 'Cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:* Published_Applications_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 21956, A Sequence 6092, Ap Sequence 11083, A Sequence 13715, A Sequence 1355, A Sequence 1835, A Sequence 1835, A Sequence 442, App Sequence 204, App Sequence 204, App Sequence 183, App
SUMMARIES	0.85-09-864-761-21956 0.85-09-864-761-21956 0.85-09-864-761-27115 0.85-09-918-995-35971 0.85-09-918-995-35971 0.85-09-918-995-35971 0.85-09-960-352-10742 0.85-10-184-644-442 0.85-10-184-644-442 0.85-10-184-644-442 0.85-10-184-644-442 0.85-09-864-761-7315 0.85-09-864-864-204 0.85-09-860-352-12395 0.85-09-860-352-12395 0.85-09-802-864-864 0.85-09-802-864-863 0.85-09-802-864-863 0.85-09-802-864-863 0.85-09-802-862-863 0.85-09-802-862-863 0.85-09-802-863 0.85-09-803-802-803 0.85-09-803-803-803 0.85-09-803-803-803 0.85-09-803-803-803 0.85-09-175-737-183 0.85-10-175-737-183
% Query Match Length DB	256 10 466 10 151 10 151 10 425 9 425 10 420 10 428 10 428 10 1594 9 1594 9
& Query Match I	00000444444444444444444444444444444444
Score	150.2 151.48 4 6.44 151.18 151.18 4 1.08 4 1.08 4 1.09 4 1.09 4 1.09 4 1.09 6 1.09 1.09 1.09 1.09 1.09 1.09 1.09 1.09
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Sequence 183, App	ň
US-10-175-752-183 US-10-176-482-183 US-10-176-482-183 US-10-176-913-183 US-10-180-552-183 US-10-180-557-183 US-10-173-700-183 US-10-174-552-183 US-10-174-552-183 US-10-174-588-183 US-10-175-740-183 US-10-175-740-183 US-10-175-740-183 US-10-176-981-183 US-10-177-981-183	01 (0) (1)
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ALIGNMENTS

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Sequence 21956, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Conf. Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THILE DOE INVENTION: GENE EXPRESSION ANALYSIS CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 CURRENT FILING DATE: 2001-05-24 PRIOR PAPLICATION NUMBER: US 60/180,312 PRIOR PELING DATE: 2000-02-04 PRIOR PELING DATE: 2000-05-26 PRIOR PELING DATE: 2000-05-26 PRIOR PELING DATE: 2000-05-26 PRIOR PELING DATE: 2000-09-03 PRIOR PELING DATE: 2000-09-03 PRIOR FILING DATE: 2000-09-27 PRIOR PELING DATE: 2000-09-27 PRIOR PELING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30 PRIOR PILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30 PRIOR PILING DATE: 2001-01-30 PRIOR PRIOR PILING DATE: 2001-01-30 PRIOR PRIOR PRIOR 
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OR APPLICATION NUMBER: PCT/USO1/00668
OR PLILNG DATE: 2001-01-30
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OR PLILNG DATE: 2001-01-30
OR FILLING DATE: 2001-01-30
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OR APPLICATION NUMBER: PCT/USO1/00661
OR FILLING DATE: 2001-01-30
-09-864-761-21956
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                          PRIOR APPLICATION NUMBER: CT/VSOL/VOUGED PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USOL/VO0664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USOL/VO0669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-31
PRIOR APPLICATION NUMBER: PCT/USO1/00666 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/USO1/00667
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 97.35
Matches 181; Conservative
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenshen
APPLICANT: Sold-05-23
CURRENT APPLICATION NUMBER: US 60/180, 312
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 ACNTIGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGACCAGTTTCAT 610
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Best Local Similarity 98.5%; Pred. No. 1.4e-47;
Matches 192; Conservative 0; Mismatches 3; Indels 0;
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: SYPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: SYPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: WILL SYPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: WILL SYPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: WILL SYPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: WILL STREAM ST
                                  PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-09-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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; Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 178; DB 10; Length 466; 97.3%; Pred No. 1.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                      OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.0 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6 USHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 6092
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N: EXPRESED IN PLACENTA, SIGNAL = 0.82
N: EXPRESED IN LUNG, SIGNAL = 0.89
N: EXPRESED IN LUNG, SIGNAL = 0.84
N: EXPRESED IN BETAL LIVER, SIGNAL = 0.96
N: EXPRESED IN BRAIN, SIGNAL = 0.96
N: EXPRESED IN BONE MARROW, SIGNAL = 0.88
N: EXPRESED IN ADULT LIVER, SIGNAL = 0.81
N: NT HIT: M18533.1, EVALUE 6.00e-80
N: SWISSPROT HIT: P11532, EVALUE 4.00e-08
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PRIOR FILING DATE: 2000-02-04

PRIOR PLING DATE: 2000-02-06

PRIOR PLING DATE: 2000-05-26

PRIOR PILING DATE: 2000-03-04

PRIOR PILING DATE: 2000-08-03

PRIOR PILING DATE: 2000-08-03

PRIOR PILING DATE: 2000-09-03

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR PILLING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLILNG DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                 Sequence 27715, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/608,408
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                    GENERAL INFORMATION
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OTHER INFORMATION:
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; OTHER INFORMATION:
US-09-864-761-27715
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                                                                                                                                      US-09-864-761-27715
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LENGTH: 151
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.88
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 11083
LENGTH: 467
                                                               TITLE OF INVENTION: OLDER LANGER REPERENCE: Acondroa-X-1; CURRENT APPLICATION NUMBER: US/09/864,761; CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR RELING DATE: 2000-05-26 PRIOR PAPLICATION NUMBER: US 69/632,366; PRIOR FILING DATE: 2000-03-03 PRIOR FILING DATE: 2000-03-03 PRIOR FILING DATE: 2000-10-04 PRIOR FILING DATE: 2000-10-04 PRIOR FILING DATE: 2000-10-04
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PRIOR FLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PLILNG DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 2001-01-30
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Gaps
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5.5%; Score 151; DB 10; Length 151; 100.0%; Pred. No. 8.8e-36;
                             Indels
                            Mismatches
5.5%,
100.0%; Pre
                         Conservative
         Best Local Similarity
Matches 151; Conserve
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TYPE: DNA ORGANISM: Bos taurus
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: MUSCLE AND PAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 CCAGACCTAATTGACATGAGAGTGTG---AAGCATAGATCCAACAAAGACAATCTGAGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 GAGGCCTTCAGAATTGCAGAACAAGAATTAAAAATCCCCAGATTGCTGGAACCAGAAGAT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CATGCATTCAACATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGAT 121
                                                                                                                          Gaps
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                                                                                                      862 AACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGA 921
                       1.7%; Score 46.4; DB 9; Length 425; 57.1%; Pred. No. 0.0017; tive 0; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35971
LENGTH: 425
                                                                                                                                                                                            922 AGACCTAAAACGCCAAGTACAACAACATAAG 952
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                                                                                                                                                                                                                                                                                                                        US-09-918-995-35971
; Sequence 35971, Application US/09918995
; Publication No. US20030073623A1
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US-09-918-995-35971
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Best Local Similarity
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874 AGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACG 933
                                                                                                                                                                                                                                                                                                                          694 AACAGGAAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATTCTCCTAAA 753
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                      Query Match 1.6%; Score 43; DB 10; Length 436; Best Local Similarity 48.6%; Pred. No. 0.019; Matches 118; Conservative 0; Mismatches 125; Indels
; OTHER INFORMATION: Clone ID: 46-LIB3058-032-Q1-K1-D10 US-09-960-352-10742
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APPLICATION NUMBER: PCT/US01/00663
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755 TCAAGATGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTT 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 423;
                                                                                                                                                                                                                                                                                    OTHER INFORMATION: MAP TO ACO10133.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.0
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN PLACEMTA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
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1.5%; Score 42.2; DB 10; Length,
Best Local Similarity 51.2%; Pred. No. 0.032;
Matches 148; Conservative 0; Mismatches 138; Indels
                                                                          PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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               PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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CURRENT FILING DATE: 2002-06-28
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Publication No. US20030044930A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2001-01-30
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Wood, William I.
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2135 GACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTG 2194
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                                                                                                                                                         1.5%; Score 41.8; DB 9; Length 440; Conservative 132; Mismatches 214; Indels
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1.5%; Score 41.8; DB 9; Length 440;
Best Local Similarity 8.7%; Pred. No. 0.044;
Matches 33; Conservative 132; Mismatches 214; Indels (
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 442
LENGTH: 440
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NUMBER OF SEQ ID NOS: 612
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Publication No. US20030068684A1
GENERAL INFORMATION:
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69 S..H.A.RHBMBCYSB..M 51
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Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                            ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-442
                                                                                                                                                       Query Match
Best Local Similarity
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PRIOR FILING DATE: 2001-01-30
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LENGTH: 425
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APPLICANT: Rank, David R.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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                                           2135 GACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTG 2194
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                                                                                                       429 GDS.WB..TACTYCM.KGKBYSWSCNN...A.CBBNGKBNRBHBSY..TTY.NSM.H.C. 370
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CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-03

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PELICATION NUMBER: US 60/207,366

PRIOR PELICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 1651.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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46.3%; Pred. No. 0.099;
tive 0; Mismatches 154; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5%; Score 41.6; DB 10; Length 557; 53.0%; Pred. No. 0.059; tive 0; Mismatches 79; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 ATCAAATGCACTAITCTCAACAGATCACGGTCAGTCTAGCACAGGGAT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 TCTAACATCACTTTTCTATACAAATCCTGCTGAGGAGTGTCCAGGCAT 383
                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 1.9
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PAPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4010, Application US/09960352
; Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: MAP TO AC008739.5
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                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
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US-09-822-846-343/c
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LENGTH: 1381
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                                                                                                         TYPE: DNA
                                                                                                                                                                                        Query Match
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
820 GGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAG 879
                                                              880 AACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGT 939
                                                                                                                                208 ACAGGAAATTAAAAAGAGCAACCATAAAGAGTCTCATGGGAGCAATGCATGAACAAACTG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    798 GCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACT 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 40.4; DB 10; Length 428; 53.1%; Pred. No. 0.11; tive 0; Mismatches 76; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                 940 ACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCA 986
                                                                                                                                                                                      858 GGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAG 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 GGACTCAAAAATTTAATGTGTCCAACAGAAGAATCGATGAAG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SOFTWARE: Corixa Invention Disclosure Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12395, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                   Sequence 204, Application US/09864864
Patent No. US20020102679A1
                                                                                                                                                                                                                                                                                                                                                                         Harlocker, Sugan L.
Dillon, Davin C.
Secrist, Heather
Lodes, Michael J.
Rigate, Paul A.
Fling, Steve P.
Mannion, Jane
Benson, Darin R.
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APPLICANT: Mitcham, Jennifer L.
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Best Local Similarity 53.19
Matches 86; Conservative
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US-09-864-864-204
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LENGTH: 428
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700 AAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAG 759
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                                                                                                                                                                                                                                                                                                           880 AACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics Institute, Inc. VENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
                                                                                                                                                                                               1.4%; Score 39.8; DB 10; Length 418;
47.1%; Pred. No. 0.17;
tive 0; Mismatches 137; Indels 0.
                                                                                                               ORGANISM: Bos taurus

) OTHER INFORMATION: Clone ID: 53-LIB3058-009-Q1-K1-F2

US-09-960-352-12395
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12395
LENGTH: 418
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CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 343, Application US/09822846 Publication No. US20030027139A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-04-06
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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Resnick, Richard J.
Gulukota, Kamalakar
Graham, James R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 ATCTAGACACAGAATCCTT 155
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                                                                                                                                                                                                                                  Matches 122; Conservative
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Merberg, David
Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wong, Gordon G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark, Hilary
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                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Xenopus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Resnick,
APPLICANT: Gulukota,
APPLICANT: Graham, J
APPLICANT: Genetics
TITLE OF INVENTION: P
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789 AAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGGGT 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 183
LENGTH: 1594
                                                                                                   0; Gaps
                                                                            789 AAAAACAAAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGT 848
                                          44; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0%; Pred. No. 0.52;
Matches 66; Conservative 0; Mismatches 44; Indels 0;
1.4%; Score 39.6; DB 9; Length 1381; 60.0%; Pred. No. 0.47; tive 0; Mismatches 44; Indels 0;
                                                                                                                                                          ; Sequence 183, Application US/10174590 ; Publication No. US20030008352A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
MPPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                           Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
          Query Match
Best Local Similarity 60.0%
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-183
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Search completed: April 25, 2003, 23:58:14 Job time : 192.615 secs

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April 25, 2003, 07:56:07 ; Search time 2252.17 Seconds (without alignments) 17070.103 Million cell updates/sec
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1321
1 cgactttccagcagttcaga.......ctaataagccagagatc 1321
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                            2054640 seqs, 14551402878 residues
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                                           OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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em_htg_rod:*
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em_htg_vrt:*
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Maximum DB seq length: 5000
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Perfect score:
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Shortened dystrophin Patent: JP 1999318467-A 2 24-NOV-1999; SCIENCE & TECH AGENCY,NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY

PAT 18-JUN-2001

linear

DNA

4402 bp

E30219

RESULT 1 E30219

E30219 E30219.1 GI:13017026 JP 1999318467-A/2. Shortened dystrophin.

DEFINITION ACCESSION VERSION KEYWORDS

unidentified. unidentified unclassified

ORGANISM

SOURCE

REFERENCE AUTHORS

1 (bases 1 to 4402) Sinichi,T.

TITLE JOURNAL

E30222 Shortened d X99700 x.laevis mR AF339032 Danio rer X99702 s.caniculua AJ23356 Strongylo X99701 x.laevis mR U43517 Scyliorhinu L05649 Homo sapien AB011666 Rattus no K59468 R.nocregicu U43520 Mus musculu X99738 pectinidae E30223 Shortened d AF339031 Danio rer M92650 Human Duche BC028720 Homo sapi X99736 B.Lanceolat M86889 H.sapiens d 899756 C.infestina 862620 (mdx3Cv)-dy M86891 H.sapiens d AF195788 Rattus no AF195787 Rattus no E30219 Shortened d X69767 R.norvegicu S38776 Homo sapten X99757 D.melanogas M8684 H.sapiens d Z11860 H.sapiens g X15488 Human mRNA L05648 Homo sapien Shortened d Shortened d Torpedo cal Shortened d X83506 M.musculus U43519 Human dystr S38777 Rattus norv score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. M868890 H.sapiens d M86888 H.sapiens d AF213441 Homo sapi M86885 H.sapiens d X99737 Asteroidea Description E30218 M37645 SUMMARIES ALIGNMENTS E30218 FSCDYSTRO E30223 AF339032 SCDYSTROP SPAJ3356 XLUTROPHI SCU43517 HUMDYSTR15 MMGUTRPH XLDYSTROP AF339031 AB011666 MMU43520 PSDYSTROP ASDYSTROP HUMDYST01 HSDYSTX60 HUMDYSTR14 BC028720 RNAPDY3 HUMDMDXX HSU43519 HUMDYST06 HUMDYST08 GSU43518 HUMDYST02 E30220 E30221 CIDYSTRO DMDYDTRO HUMDYST07 E30219 AF213441 RNADYI HSDYSRP 10 Query Match Length DB 10 07 4402 4402 4075 3650 1482 1428 500 1737 1961 1195 384 1428 1105.2 906 770.4 Score 766.2 737.6 712.6 619.2 604 604 577.8 555 551.8 544 493.8 410.4 379.4 375 265 241.8 241.6 203 191.8 179.8 161.2 157 153.2 369.8 221.6 208.6 151 83.8 83.8 82.2 82.2 149 122 94 Result

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   892 GGACCAGCACACACACACAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTG 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       832 AAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTT 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712 TATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            772 GTCTTTAGCTGACTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCG 831
                                                                                                                                                                                                                                                                                                                                                                                        1878 TGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGC 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 CCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGA 591
                                                                                                                                                                                                                                                                                                           1818 TGAGTGGGAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCT 1877
                                                                                                                                                                                                                                                                         1758 TGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAGGAGGTCAATAC 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                    412 TCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAG 471
                                                                                                                                                                                                                                                                                                                                             292 TGAAAGACTCCAAGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGC 351
                                                                                                                                                                                                                                                                                                 232 TGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGACACCCT 291
                                                                                                                                                                                                                                                    172 TGAGGAGAGACCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATAC 231
                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                         83.7%; Score 1105.2; DB 6; Length 4402; 97.6%; Pred. No. 4.9e-311; tive 0; Mismatches 28; Indels 0;

    4402
    /organism='Unidentified'.

                                                                                                 Location/Qualifiers
                                                                                                                                                                    /db_xref="taxon:32644"
1000 c 1019 g 1054 t
                                                             C12N15/09, A61K48/00, C12N15/00 Strandedness: Both;
                                                                                                                                                  1. .4402
/organism="unidentified"
                              08-MAY-1998 JP 1998142134
                                                                                                                                   Location/Qualifiers
                                                                                           Topology: Linear;
           JP 1999318467-A/2
                                                        SINICHI TAKEDA
                                                                                                                                                                                                                                        Conservative
Unidentified
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Matches 1122; Conserv
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PAT 18-JUN-2001
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Patent: JP 1999318467-A 3 24-NOV-1999;
SCIENCE & TECH AGENCY,NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
OS Unidentified
PN JP 1999318467-A/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1252 CTTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAA 1311
2838 CTTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTGCTAATAATAA 2897
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                                                                                                                                        1072 GATCCGTGTCCTGTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGA 1131
2478 GGACCAGCACAACCTCAAGCAAAATGACCAGGCCCATGGATATCCTGCAGATTATTAATTG 2537
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Strandedness: Both;
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984 c 1010 g 10
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1 (bases 1 to 4402)
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Matches 906; Conservative
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                                                            536 AGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGA 595
                                                                                                                                                                                                       2302 AACCACGAGACTCAAACATGCTGGGACCATCCCAAAATGACAGGGGCTCTACCAGTCT 2361
                                                                                                                                                                                                                                                    476 GTCAATGACCTTGCTGGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTC 535
                                                                                             2482 CAGCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATATTATTAATTGTTTG 2541
                                                                                                                                                                                                                                                                                                                                                                                   956 ACCACTATTTATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTCTGC 1015
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                                                                                                                                                                                         716 AACCACGAGACTCAAACAACTIGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCT 775
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Shortened dystrophin
Patent: JP 1999318467-A 4 24-NOV-1999;
SCIENCE & TECH AGENCY,NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602 CAGCIGCAIGAAGCCCACAGGGACTTIGGICCAGCAICTCAGCACTITCTICGACGICT 661
                                                                                                                                                                                                                                                                                                                                                                      662 GTCCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCAC 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         962 ATTTATGACCGCCTGGAGCAAAGGACACAATTTGGTCAACGTCCCTCTCTGCGTGGAT 1021
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                                                                                                                                                                                                                                         Match 58.3%; Score 770.4; DB 6; Length 4075; Local Similarity 99.2%; Pred. No. 2.6e-213; les 774; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                          'organism='Unidentified'
                                                                                                                                     Location/Qualifiers
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                                                                                                 C12N15/09, A61K48/00, C12N15/00
Strandedness: Both;
                                                                                                                                                                                      /organism="unidentified"
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910 c 936 q
                                                                  08-MAY-1998 JP 1998142134
                                                                                                                                                                   Location/Qualifiers
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                                 Unidentified
JP 1999318467-A/4
24-NOV-1999
                                                                                                                        Topology: Linear;
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PAT 18-JUN-2001

linear

DNA

4075 bp

Shortened dystrophin. E30221 E30221.1 GI:13017028

E30221

DEFINITION

RESULT 3 E30221 LOCUS ACCESSION VERSION KEYWORDS

JP 1999318467-A/4. unidentified. unidentified

ORGANISM

SOURCE

unclassified. 1 (bases 1 to 4075)

Sinichi, T.

REFERENCE AUTHORS

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SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               963 TTTATGACCGCCTGGAGCAAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATA 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 TGGAAGACCTGAACACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 602
           1262 AGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAAGCCAGAGATC 1321
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Pred. No. 4.4e-212;
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Strandedness: Both;
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/organism="unidentified"
/db_xref="taxon:32644"
853 c 859 g 92.
                                                                                       3747 bp
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                                                                                                                                                                                                                                                                                                                                           Topology: Linear;
                                                                                                                        E30218.1 GI:13017025
                                                                                                Shortened dystrophin. E30218
                                                                                                                                                                                   (bases 1 to 3747)
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/ ...____SGEQWRLQISLQDFLTWMNLKNDELRRQMPIGGDAPTVCQQND //Lranslation="SGEQWRLQISLQDFLTWAPIRAPESLLTGPREKIPEENIQNVAKRI VHRIFKRELKAKEPVWRSALDTVHLFLADPAIRAPESLLTGPREKIPEENIQNVAKRI VHRIFKRELKAKEPVWRSKURNSVDWQKRIDEALKRLLELQDSMDELNIKLRQARAIKDTWQP RCBLLIDSLQDHIEKVKVFRAEIAPWKENVTHMNDLASQFTPPDIQLSPYNLNQLEDL VTRWKLLQVSIDELLKQLHEAHRDFGPTSQHFLSTSVQGPWERAISPNKVPYYINHQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted by S.J. Burden, 06-AUG-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Eukaryota; Metazoa; Butoidea; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo. 1 (bases I to 2654) Per, 2654) Dyer, S.M. and Burden, S.J. Yeadon, J.E., Lin, H., Dyer, S.M. and Burden, S.J. Cell Biol. 115 (4), 1069-1076 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear VRT 08-SEP-1993
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Multiple dystrophin isoforms are associated with the postsynaptic
membrane of Torpedo electric organ
J. Physiol. (Paris) 85 (3), 131-133 (1991)
                                                                                                                                                                                                                                   1203 TICTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCA 1262
                                                                                                                                                  1083 TGTCTTTTAAAACTGGCATCATTTCCCTGTAAAGCACATTTGGAAGACAAGTACAGAT 1142
                                                                                                                                                                                                                                                                                                                                           2015 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGAT 2074
1023 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 1082
                                                                                       On Sep 8, 1993 this sequence version replaced gi:213232
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Torpedo californica dystrophin mRNA, 3' end.
M37645
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/protein_id="AAC38002.
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842 AAGGCCCTTTGGTTCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCAC 901

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902 AACCICAAGCAAAAIGACCAGCCCAIGGAIAICCIGCAGAITAITAAIIGIIIIGACCACI 961

1082 CTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGA 1141 QQ

1142 TACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTC 1201

QTTCWDHPKWTELYQSLADLNNVRFSAYRTAMKLRRLQKALCLDLLSLPSACEAFDQH ; 0 105 GATGCTCCCACAGTCTGTCACAGAACGATGTTCACCGAATTTTCAAGCGAGAGTTGAAG 164 62 ACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAG 121 165 GCAAAGGAACCAGTGGTCATGAGCGCTTTGGACACAGTGCATTTGTTCTTGGCTGATCA 224 0; Gaps 122 CCITTGGAAGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGA 181 225 GCAATCAGAGCTCCTGAAAGTCTTTTAACTGGACCAAGAGAAAAATACCTGAAGAGAAC 284 182 GCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAA 241 242 AAATTGAACCTGCACTCCGCTGACTGGCAGAAAAATAGATGAGACCCTTGAAAGACTC 301 2 GACTITCCAGCAGTICAGAAGCAGAACGATGTACATAGGGCCTICAAGAGGAATIGAAA 61 302 CAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATC 361 362 AAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCCAAGATCACCTCGAG 421 422 AAAGTCAAGGCACTICGAGGAGAAATIGCGCCTCTGAAAGAAGAACGIGAGCACGTCAAT 481 482 GACCITGCICGCCAGCITACCACITIGGGCATICAGCICTCACCGIATAACCTCAGCACT 541 585 GATCTCGCTTCCCAGTTCACCACCTGATATCCAATTATCCCGTACAATCTAAACCAG 644 542 CTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGG 601 55.8%; Score 737.6; DB 5; Length 2654; 72.4%; Pred. No. 9.5e-204; tive 0; Mismatches 364; Indels 0; 646 g Matches 956; Conservative Similarity 773 a Query Match Local BASE COUNT ORIGIN

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linear PAT 18-JUN-2001 ó Sinichi, T.
Shortened dystrophin
Patent: JP 199918467-A 6 24-NOV-1999;
SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
OS Unidentified 0; 53.9%; Score 712.6; DB 6; Length 3163; 98.8%; Pred. No. 1.9e-196; Indels 'organism='Unidentified'. Location/Qualifiers DNA 782 t Mismatches C12N15/09, A61K48/00, C12N15/00 1. 3163 /organism="unidentified" /db_xref="taxon:32644" a 731 c 720 g 782 3163 bp Location/Qualifiers Strandedness: Both; 0; Topology: Linear; Shortened dystrophin. E30223 E30223.1 GI:13017030 (bases 1 to 3163) SINICHI TAKEDA JP 1999318467-A/6. Conservative unidentified. unidentified unclassified. Source Similarity 930 a E30223 718; PD PR PC CC CC CC FH Query Match DEFINITION ACCESSION VERSION source ORGANISM REFERENCE BASE COUNT RESULT 6 AUTHORS JOURNAL KEYWORDS Matches TITLE COMMENT FEATURES ORIGIN

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Dystrophin and Dp71, two products of the DMD gene, show a different pattern of expression during embryonic development in zebrafish Mech. Dev. 102 (1-2), 239-241 (2001)
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( pases 1 to 3521)

1 ( pases 1 to 3521)

Bolanos-Jimenez, F., Bordais, A., Behra, M., Strahle, U., Sahel, J. and
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                                                               895 CCAGCACAACCTCAAGCAAAATGACCCAGCCCATGGATATCCTGCAGATTATTAATTGTTT 954
               942 AGCCATCCAGGAAGTGGAAGCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTGTTC 1001
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                                                                                                                                                                          775 TTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAG 834
                                               715 CAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGGGCTCTACCAGTC
AF339031.1 GI:13699249
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NEKLESHKKYSHSVEDEKGONADUKOLSKDIQOMOTOMNVTNELANKILITEVADDOTS
KVOATESHNILAMAI KRKÄÖK BADLEAGLEROLOHYYLDIEKFINMILTEAETTANVL
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VSPEERVONVGRILEREVEDYVTRKKNILGARAVDMOGOLEDALEMMELOLOHOOADOLUDY
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LMRVAAAETAKHQAKCNICKEKPTKRYFAKHPRMGYLPVQTILEGDNMETPVTLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="RECRHWEDSHAKLTARVLTLQNMYKDSSDWLEARKRVEPLIKKA
                                                      Direct Submission
Submitted (22-JAN-2001) Laboratoire de Physiopathologie Retinienne,
EMI 99-18 INSERM-Universite Louis Pasteur, 1, Place de l'Hopital,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081 GAATCTGGGGTGCAGCTTCTTGTGGACTGGCAGCAACAGCTGGAACTGGCCTTGGAGAGGCT 1140
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2 (bases 1 to 3521)
Bolanos-Jimenez,F., Rendon,A. and Strahle,U.
                                                                                                                                                                                                                                                                                               /map="between z5508 and z5058"
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A 71-Kilodalton protein is a major product of the Duchenne muscular dystrophy gene in brain and other nonmuscle tissues Proc. Natl. Acad. Sci. U.S.A. 89 (12), 5346-5350 (1992)

/organism="Homo sapiens" /db_xref="taxon:9606" /map="Xp21.3-p21.1" /cell_type="amniotic fluid"

Location/Qualifiers 1. .2110

1319059

JOURNAL PUBMED

TITLE

source

FEATURES

/tissue_type="brain" 1. .2110

/gene="DMD"

5'UTR

gene

/note="G00-119-850"

/gene="DMD"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2110)
Lederfein,D., Levy,Z., Augier,N., Mornet,D., Morris,G., Fuchs,O., Yaffe,D. and Nudel,U.

sapiens brain cDNA to mRNA.

Homo sapiens

ORGANISM

SOURCE

REFERENCE AUTHORS

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1261 CAGAGTGAAGGCATTTCAGGAAGAGATAGCTCCCATTCAGGATAACGTAAATCATGTTAA 1320
                                                                                                                                                                                                                                                                                421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAAGGTGAGCCACGTCAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1021 TATGTGTGTGTAACTGGCTGGTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             901 CAACCICAAGCAAAAIGACCAGCCCAIGGATAICCIGCAGAITATAAITGIIIGACCAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1201 CCTICTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260
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Translation="WREGLKGHETQTTCWDHPKMTELYQSLADLNNVRFSAYRTAMKL
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.1921

CDS

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PPQDTSTGLEEVMEQLNNSFPSSRGHNVGSLFHMADDLGRAMESLVSVMTDEEGAE"
                                                                                                                                                                                                                                                                                                                                                                                                                  958 CACTATITATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTCTGCGT 1017
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                                                                                                                                                                                  718 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 777
                                                                                                                                                                                                778 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 837
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                                                                                                                                45.7%; Score 604; DB 9; Le
100.0%; Pred. No. 9.2e-165;
                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 9.20
Matches 604; Conservative 0; Mismatches
                                                                        /note="G00-119-850"
                                                                                         492 g
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linear PRI 07-NOV-1994

HUMDMIXX
2110 bp mRNA linear PRI 07-HUMBA Duchenne muscular dystrophy (DMD) mRNA, complete cds. M92650

Duchenne muscular dystrophy protein.

M92650.1 GI:181598

HUMDMDXX

DEFINITION ACCESSION

KEYWORDS VERSION

RESULT 8 HUMDMDXX

LOCUS

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ROD 23-AUG-1995
                                                                                                                                                                      LEPOSMYMLEVALHEYARAAETAKHQAKCNICKECPIIGERYRSLKHFNVDICQSCFFSG
LEPOSMYMLEVALHRYARAAETAKHQAKCNICKECPIIGERYRSLKHFNVDICQSCFFSG
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CDQRRLGLLLHDSIQIPRQLGEVASFGGSNIEPSVRSCEQFANNKPEIEAALFLDWMR
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100.0%; Pred. No. 1e-164;
tive 0; Mismatches 0; Indels
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                  /protein_id="AAH28720.1"
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Becker types)"
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X83506.1 GI:793851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             According appears the property of the property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
TOSHiyuki and Piero Carninci (RIKEN)
GDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4658)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (29-APR-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.systemsblology.org
contact: amadan@systemsblology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                         1258 GGGCAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAAGCCAGA 1317
                                                                                                                                                                                                                                                                                                          1198 CCTCCTTCTGCATGALTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGG 1257
                                                                            1078 IGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1137
                                                                                                                                                                                        1138 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCAGGCTGGG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                        553 CCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGG 612
                                                                                                                                                                                                                          373 GGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
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/clone_lib="NIH_MGC_97"
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/db_xref="taxon:9606"
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/Translation="Woller" | Vitable | Vi
                                                                                                                 Eukaryott; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Blake, D.J., Schofield, J.N., Zuellig, R.A., Gorecki, D.C., Grhofield, J.N., Zuellig, R.A., Gorecki, D.C., Gutrophin, the autosomal homologue of dystrophin Dpl16, is Proc. Natl. Acad. Sci. U.S.A. 92 (9), 3697-3701 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHDDTHSRIEQYATRLAQMERTNGSFLTDSSSTTGSVEDEHALIQQYCQTLGGESPVS
QPOSPAQILKSVEREERGELERIIADLEEEQRNLQVBYEQLKEQHLRRGLPVGSPPVS
IVSPHHTSEDSELIADAKLLRQHKGRLEARMQILEDHNKQLESQLHRLRQLLEQDDSD
SRINGVSPWASPQHSALSYSLDTDPGFPQFHQAASEDLLAPPHDTSTDLTDVMEQINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-DEC-1994) D.J. Blake, Institute of Molecular Medicine, Molecular Genetics, John Radciiffe Hospital, Oxford, Oxfordshire OX3 9DU, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Gaps
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/protein_id="CAA58496.1"
/db_xref="G1:793852"
/db_xref="MGD:MG1:104631"
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/clone_lib="adult mouse brain"
/dev_stage="adult"
1. .197
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/clone="AU#3"
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                            753 CCAATAGAGGCCCCCGAAGAACAAGAAGAAACCCACAATCAAAGACAGAGAGTTGACTCCT 812
                                                        173 GAGGAGAGACCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACT 232
                                                                          233 GAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTT 292
                                                                                                                                                                                            873 AAGTGGGAAAATCTAAATGCTGTCACTAGCAACTGGCAAAAGCAAGTAGGGAAGGCGTTA 932
                                                                                                                                                                         293 GAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGGTGCGCCAAGCT 352
                                                                                                                                                                                                                                   353 GAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCCAAGAT 412
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DB 9;
                   42.0%; Score 555; DB 9,
64.0%; Pred. No. 2e-150,
                                                               Matches 837; Conservative
                                             Similarity
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ELRKWQHESARAPSLADGSTEAATDHRNEELLAGARILKQHKSRLETRMQILEDH
NKQLESQLQRLRELLLQPPTESDGSCSAGSSIASSPQOSEGSHPREKGQTTPDTEAAD
9VGSKSQPVSLCLEDIMEKLRHAFPSVRSSDVTANTLLAS"
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APLOLPLOBIIDWISGKDEELSAQLPLOGDVALVQOEKETHAAFMEEVKSRAPYIYSVI
ESAQAFLSQHPFEELEEPHSESKOTSPKORIONISFWWKQATVASELBMEKITARCVD
ESAQAFLSQHPFEELEEPHSESKOTSPKORIONISFWWKQATYASELBMEKITARCVD
EFFSPRKDGVLETGGAMEELSTTISGAEGVRAFFPIGDLFIDSLPBHIQAIKLFR
BEFSPRKDGVLVANDLAHQLAISDVHISMENSQALEQIINTRWCQLQASVDFRLKQLQD
ARRDGGGGGHFLSSSVQVPWERAISPNKVPYYINHQAQTTCWOHPKMTELYQTLADL
NNIKFSAYRTAMKLRRVQKALRLDLYTITTALEFFNEHDLQASSHVMDVVEVIHGLTA
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LQYLFSQVANGSGODRHLGVLHBAIQVPRQLGEVVAAFGGSNVEPSVRSCFRFSTG
KPVIEAGFLEWVNLEPQSMVWLPVLHRVTIAEQVKHQTKCSICRQCPIKGFRKYRSLK
QFNVDICQTCFLTGRASKGNKLHYPIMEYYTPTTSSENMRDFATTLKNKFRSKHYFSK
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                                                                                                                                                                                                                                                               PRI 15-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 263 to 3189)

Roberts, R.G., Freeman, T.C., Kendall, E., Vetrie, D.L., Dixon, A.K., Shaw-Smith, C., Bone, Q. and Bobrow, M.

Characterization of DRP2, a novel human dystrophin homologue Nat. Genet. 13 (2), 223-226 (1996)
                                                   1833 CTTGGCCTGCTACTTCACGATGCCATCCAGACTGGGGGAAGTAGCAGCC 1892
                                                                                                                                                                                                                                                       HSU43519 3499 bp MRNA linear PRI 15-JUI
Human dystrophin-related protein 2 (DRP2) MRNA, complete cds.
043519
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Submitted (16-DEC-1995) Roland G. Roberts, Medical Genetics,
Addenbrooke's Hospital, 3rd Floor, Lab Block, Addenbrooke's
Hospital, Hills Road, Cambridge, Cambs Cb2 20q, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="dystrophin-related protein 2"
/protein_id="AAC50538.1"
/db_xref="G1:1353782"
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/chromosome="X"
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HSU43519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                854 ITGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAA 913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       674 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACA 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 CAGCCCGIGGGCGATCICCICATIGACICICCCAAGAICACCICGAGAAAGICAAGGCA 433
                                                                                                                                                                                                                                                                                                                                                                                        254 CACTCCGCTGACTGGCAGAAAAAAAAAAGACCCTTGAAAGACTCCAGGAACTTCAA 313
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                                                                                                                                                                                                                                                                                                                                      74 GTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGA 133
                                                                                                                                                                                           790 TACATCTATTCTGTGCTGGAGTCAGCTCAGGCCTTCCTGTCCCAGCACCCATTTGAGGAG 849
                                                                                                                                                                                                                                 850 TTAGAGGAGCCTCATTCTGAGAGCAAAGATACCTCCCCGAAACAGCGGATCCAGAATCTC 909
                                                                                                             730 GIGCAACAGGAGGAGGAGACACATGCGGCCTTTATGGAAGAAGTCAAGTCTCGGGCCCCC 789
                                                                       14 GITCAGAAGCAGAACGAIGTACATAGGGCCTTCAAGAGGGAATIGAAAACTAAAGAACCT 73
                                     Gaps
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Length 3499;
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ROD 02-MAY-2001
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Roberts, R.G. and Sheng, M.
Burnet submission
Direct submission
GKT Medical School, 8th Floor, Guy's Hospital, Guy's Tower, London
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Translation="MOPLWOGCPYTLPRCHEWHAADREHHSSSLRNTCPQPQVRAAV TIPAPPWDGAGDPCLEWEKLMGSVQAVGLEPSAMNLCWNETRKKSHURRARLEAFSD SYLESAPLDGETOTALVQQERETHAAFMEEVRESDESDCLESAQLPLQGEDVALVQQERETHAAFMEEVRSKGPYIY CVDQHRHEHTLEHLLENGEBESBESKDTSPRQRIONLSRFVWKQATVASELWEKLTAR LEKEEFSPVKDGVKLVNDLAHQLAISDVHLSMARTWEPIGDLFIDSLPEHIQAIK
1034 FGGCTGCTGAAFGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTTAAA 1093
                   1750 TGGCTCCTCAATGTTTTGATAGTGGTCGCAGCGGAAAGATGCGGGCATTGTCTTTTTAG 1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                      1094 ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 1153
                                                                                                       1810 ACTGGCATTGCATGCTTGTGTGGCACGGAAGTGAAGGAAACTTCAGTACCTCTTCAGC 1869
                                                                                                                                          1154 CAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGAT 1213
                                                                                                                                                              1214 TCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGGAGTAACATTGAG 1273
                                                                                                                                                                                                                                    /note="spiice acceptor AG dinucleotide used by A-form"
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Rattus norvegicus dystrophin-related protein 2 B-form splice
ARIJSTRR
ARIJSTRR
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Roberts, R.G. and Sheng, M.
Association of dystrophin-related protein 2 (DRP2) with
                                                                                                                                                                                                                                                                                     1274 CCAAGIGTCCGGAGCTGCTTCCAATTTGCTAATAATAAGCCAGAGAT 1320
                                                                                                                                                                                                                                                                                                        postsynaptic densities in rat brain
Mol. Cell. Neurosci 16 (5), 674-685 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/db_xref="G1:11066167"
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LODAHRDFGPGSOHFLSTSVQVPWERAISPNKVPYYINHQAQTTCWDHPKMTELYQTL
LTALYERLEEBERGALLVNVPLCVTLTTALEIPNBHDLQASEHVWDVENTHC
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KEKLQYLFSQVANSGSKCDORHLGALLHEATQVPRQLGEVAARGGSNVEPSVRSCFRF
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EDHHKQLESQLQRFREILLQPPTSDGNGSAGSSLASSPRQSEGSHPREKGQTTPDTE
AADDVGSKSQDVSHSLEDINGSFRRAFFRAFSSTANATLLAEARILLQPPTER
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                                                                                                                                                                                                                                                                                                                                                     134 CTAGAGAAACTCTACCAGGGGCCCAGAGGCTGCCTCCTGAGGAGAGAGCCCAGAATGTC 193
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                                                                                                                                                                                                                                           14 GTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCT 73
                                                                                                                                                                                                                                                                                                                                                                                                            194 ACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                      791 AGTCGCTTTGTGTGGAAGCAGGCAACAGTGGAGTGGAACTGTGGGAGAAGCTGACAGCC 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 CACTCCGCTGACTGGCAGAAAAAAAAAGATGAGACCCTTGAAAGACTCCAGGAACTTCAA 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 CAGCCCGTGGGCGATCTCCTCATTGACTCTCCAAGATCACCTCGAGAAAGTCAAGGCA 433
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                                                                                                                                                                                            41.8%; Score 551.8; DB 10; Length 3073; 63.9%; Pred. No. 1.7e-149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROD 02-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //note="DRP2; membrane-associated cytoskeletal protein;
contains two spectrin repeats; WW domain; ZZ domain"
/codon_start=1
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                                                                                                                                                                                                                        1094 ACTGGGATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 1153
                                                                                                                                                                                                  1034 IGGCIGCIGAAIGITIAIGAIACGGGACGAACAGGGAGGAICCGGIGTCCTGTCTTIAAA 1093
                                                                                                                                                                1571 CTGGAGGAGGAGAAAGAGGCATCCTGGTCAACGTGCCGCTGTGTAGACATGAGCTCAAC 1630
                                                                                                1511 AGIGAACAIGIAAIGGAIGIGGIGGAGGICAIICACIGCIIGAACGCTIGIAIGAACGA 1570
                                                                                                                                 974 CTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTGTCTGAAC 1033
                                1451 TIGGAICTGGIAACTTIAACTACAGCICIGGAGAICTICAAIGAGCACGACTIGCAGGCC 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stav bp mRNA linear ROD 02-MA variant (Drp2) mRNA, complete cds.
                                                                 914 AATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGC 973
854 ITGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roberts, R.G. and Sheng, M. Association of dystrophin-related protein 2 (DRP2) with Association of dystrophin rat brain postsynaptic densities in rat brain Mol. Cell. Neurosci. 16 (5), 674-685 (2000)
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/db_xref="taxon:10116"
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Roberts, R.G. and Sheng, M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    861 TCTTGAGCCTGTCAGCTGCGTGTGATGCCTTGGACCAGCAGCAGCTCAAGCAAAATGACC 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1161 CAAGTTCAACAGGATTTTGTGACCAGGGCGGGGGGCGTCCTTCTGGATGATTCTATCC 1220
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Similarity 90.6%; Pred. No. 2.8e-147; Length 1240;
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/protein_id="CAA49423.1"
/db_xref="GI:57914"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 t
                                                                                                                                                                                                                                 /db_xref="SPTREMBL:005485"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0, Mismatches
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                                                                         /dev_stage="neonatal"
106. .1128
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JP 1999318467-A/5.
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1338 TGGGAAAGAGAATTTCTCCCCAATAAAGTCCCCTACTACATCAACCACCAGGCTCAGACC 1397
                                                                                 Eukaryota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                    734 ACTIGCIGGGACCAICCCAAAAIGACAGAGCICTACCAGICITTAGCIGACCIGAAIAAI 793
                                                                                                                                                                 794 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGC 853
                                                                                                                                                                                                                                                                                                                                                                                                                 974 CIGGAGCAAGAGACACAATITGGICAACGICCCICTCTGCGIGGATAIGIGTCIGAAC 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1034 TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTAAA 1093
                                                                                                                                                                                                                                                                       854 TIGGATCICTIGAGCCIGICAGCTGCAIGTGAIGCCITGGACCAGCACAACCTCAAGCAA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1094 ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 1153
                                                                                                                                                                                                                                                                                                                                                                                   914 AATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGC 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 CAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCAGGCTGGGCCTCCTTCTGCATGAT 1213
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/db_xref="taxon:10116"
/cell_line="Schwannowa cells"
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DEFINITION ACCESSION VERSION

RESULT 14

RNAPDY3

ORGANISM

KEYWORDS

TITLE JOURNAL

REFERENCE AUTHORS AUTHORS TITLE

REFERENCE

source

FEATURES

MEDLINE PUBMED

JOURNAL

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                                         Shortened dystrophin
Patent: JP 199918467-A 5 24-NOV-1999;
SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
                                                                                                                                                                                                                                                                                                                         885 ATGCCTTGGACCAGACCACCAGCAAAATGACCAGCCCATGGATATCCTGCAGATTA 944
                                                                                                                                                                                                                                                                                    825 AACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTG 884
                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                37.4%; Score 493.8; DB 6; Length 3172; 99.6%; Pred. No. 1.4e-132; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                         'organism='Unidentified'
                                                                                                                                                         Location/Qualifiers
                                                                                                                           C12N15/09, A61K48/00, C12N15/00
Strandedness: Both;
                                                                                                                                                                                                 1. .3172
/organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: April 25, 2003, 14:28:17
Job time : 2282.34 secs
                                                                                                                                                                                                                 /db_xref="taxon:32644"
730 c 718 9
                                                                                                 08-MAY-1998 JP 1998142134
                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1661 ATAATAAGCCAGAGATC 1677
                                                                                 JP 1999318467-A/5
24-NOV-1999
                                                                                                                                                    Topology: Linear
                           (bases 1 to 3172)
                                                                                                                        SINICHI TAKEDA
                                                                                                                                                                                                                                                                        Matches 495; Conservative
                                                                           Unidentified
                                                                                                                                                                                                                                                                  Similarity
unidentified.
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                                       Sinichi, T.
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             ORGANISM
                               REFERENCE
                                          AUTHORS
                                                           JOURNAL
                                                                                                                                                                                          FEATURES
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Human dystrophin m
Adeno-associated v
Adeno-associated v
                                                                                                                                                                                             (without alignments)
16150.348 Million cell updates/sec
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21. $\text{SIDS2/gcgdata/geneseq/geneseqn-embl/Na1981.DAT:*}

22. $\text{SIDS2/gcgdata/geneseqr-embl/Na1981.DAT:*}

33. $\text{SIDS2/gcgdata/geneseqr-embl/Na1981.DAT:*}

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36. $\text{SIDS2/gcgdata/geneseqr-embl/Na1981.DAT:*}

37. $\text{SIDS2/gcgdata/geneseqr-embl/Na1991.DAT:*}

38. $\text{SIDS2/gcgdata/geneseqr-embl/Na1991.DAT:*}

39. $\text{SIDS2/gcgdata/geneseqr-embl/Na1991.DAT:*}

31. $\text{SIDS2/gcgdata/geneseqr-embl/Na1991.DAT:*}

32. $\text{SIDS2/gcgdata/geneseqr-embl/Na1991.DAT:*}

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                                                                                                                                                         April 25, 2003, 07:25:57 ; Search time 184.2 Seconds
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                 US-09-845-416-10_COPY_1800_3120
                                                                                                      - nucleic search, using sw model
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Listing first 45 summaries
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AAD37232
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AAD37259
AAD37258
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human dystrophin rod, hinge and CR domain regions encoding DNA #2.
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Mon Apr 28 09:28:22 2003

repeats, H1 and H4 domains and a cysteine rich domain of

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression scontrol element, in a recombinant adeno-associated virus or retrovirus is control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy hand fragment encoding rods R23 and R24, hinge H4 and CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 GCAGCIGCATGAAGCCCACAGGGACTIIGGICCAGCAICICAGCACITICITICCACGIC 660
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                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 1321; DB 24; Length 1821;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                          Sequence 1821 BP; 506 A; 451 C; 447 G; 417 T; 0 other;
                                    Example 1; Page 52-53; 71pp; English.
              dystrophin gene -
                                                                                                                                                                                                                                       domain regions.
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
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                                                                                           901 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATAATTGTTTGACCAC 960
                                                                                 841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCA 900
                                                         883 IGACCIGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human dystrophin rod, hinge and CR domain regions encoding DNA #1.
                                   781 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA
AAD37232 standard; DNA; 2169 BP.
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
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Example 1; Page 45-46; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control control element. The dystrophin minigene in operable linkage with an expression useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human an all and a second of the second of

Gaps 100.0%; Score 1321; DB 24; Length 2169; 100.0%; Pred. No. 0; tive 0; Mismatches 0; Indels 0; Sequence 2169 BP; 623 A; 529 C; 524 G; 493 T; 0 other; Matches 1321; Conservative Local Similarity Query Match ò

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601 GCAGCIGCAIGAAGCCCACAGGGACTIIGGICCAGCAICTCAGCACTIITCIITCCACGIC 660

TGTCCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 720

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1111 TGTCCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 1170 721 CGAGACTCAAACAACTIGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTAGC 780 1021 TATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1080 781 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840 1081 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140 1141 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGCGAGGCTGGGCCT 1200 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260 1651 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1710 1261 CAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAAGCCAGAGAT 1320 841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 901 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 961 TATTIATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTGCGTGGA 1321 C 1321 1771 C 1771 1201 ρp ΩŸ οq δ qq QQ δ ŏ qq òγ qq qq ò Qγ П δ g ŏ q δŏ pp ó Pp

AAD37240 standard; DNA; 3510 BP. 21-AUG-2002 (first entry) AAD37240;

RESULT 3 AAD37240

Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Human dystrophin minigene delta3510. Becker muscular dystrophy; ds.

Homo sapiens.

WO200183695-A2.

27-APR-2001; 2001WO-US13677. 08-NOV-2001.

28-APR-2000; 2000US-200777P

(XIAO/) XIAO X.

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WPI; 2002-049342/06.
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin game, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domains and cysteine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control element, in a mammal in operable linked with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3510 containing nucleotides 1-1668 (N-terminus, hinge H1 and rods R1 and R2), 8407-10227 (rods R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids). New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a Example 1; Page 51-52; 71pp; English. dystrophin gene ·

0; Gaps 100.0%; Score 1321; DB 24; Length 3510; 100.0%; Pred. No. 0; 0; Indels Sequence 3510 BP; 1073 A; 787 C; 828 G; 822 T; 0 other; 0; Mismatches Best Local Similarity 100.0%; Matches 1321; Conservative (Query Match

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181 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 240 1899 g ò

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361 CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTTCATTGACTCTCTCCAAGATCACCTCGA 420

421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAGGTGAGCCACGTCAA 480

> g ò

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Dp

27-APR-2001; 2001WO-US13677

Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds. 1081 CCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140 1141 ATACCTTTTCAAGCAAGTGGGAAGTTCAACAGGATTTTGTGACCAGGGAGGCTGGGCCT 1200 1021 TATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1080 2859 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 2918 961 TATTTATGACCGCCTGGAGCAAGAGCAACAATTTGGTCAACGTCCCTCTCTGCGTGGA 1020 781 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840 841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 900 901 CAACCICAAGCAAAAIGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 721 CGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC Human dystrophin minigene delta3531. AAD37238 standard; DNA; 3531 BP. 21-AUG-2002 (first entry) WO200183695-A2. Homo sapiens. 3099 C 3099 1321 C 1321 AAD37238; RESULT 4 AAD37238 qq QΥ op O δy g δ δ qq qq δ q QQ δ q δλ pp οy

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3531 containing nucleotides 1-1341 (N-terminus, CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                        New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                           Example 1; Page 50-51; 71pp; English.
  28-APR-2000; 2000US-200777P.
                                                                                                                      WPI; 2002-049342/06
                                                                                                                                                                                                                         dystrophin gene -
                                        (XIAO/) XIAO X.
                                                                               Xiao X;
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Sequence 3531 BP; 1071 A; 809 C; 824 G; 827 T; 0 other;

0; Gaps 100.0%; Score 1321; DB 24; Length 3531; 0; Indels 0; Mismatches Pred. No. 0; Best Local Similarity 100.0%; Matches 1321; Conservative (Local Similarity Query Match

1 CGACTITCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAAITGAA 60

61 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGGGA 120

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181 AGCCCAGAAIGTCACTCGGCTICTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 240

421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCCACGTCAA 480

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481 TGACCTIGCTCGCCAGCTTACCACTTTGGGCALTCAGCTCTCACCGTATAACCTCAGCAC 540

541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG

2340 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG 2399 2520 CGAGACTCAAACATGCTGGGACCATCCCAAAATGACAGGGGGTCTACCAGTCTTTAGC 2579 961 TATTTATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTGCGTGGA 1020 1021 TATGIGICTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1080 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140 721 CGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTAACCAGTCTTTAGC 780 2880 CCTGTCTTTAAAACTGGCATCATTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 2939 1141 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCAGGCTGGGCCT 1200 1201 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260 781 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 901 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 1321 C 1321 3120 C 3120 qq QQ δ δ q Ω Dp δλ g ò qq οχ qq QY Op à q qq δ δ à Dp QQ ά

Human dystrophin minigene delta3849. AAD37237 standard, DNA; 3858 21-AUG-2002 (first entry) AAD37237; RESULT 5 AAD37237

Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.

Homo sapiens.

WO200183695-A2.

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a mammalian adostrophy (DMD) and Becker muscular dystrophin minigene muscular dystrophy (DMD) and Becker muscular dystrophin minigene elita3849 containing nucleotides 1.1668 (N-terminus, hinge HI and rods RI, R2), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2427 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 2486
                                                                                                                                                                                       New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 2366
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                             Example 1; Page 48-49; 71pp; English.
                               27-APR-2001; 2001WO-US13677.
                                                           28-APR-2000; 2000US-200777P.
                                                                                                                                                                 WPI; 2002-049342/06.
                                                                                                                                                                                                                                                   dystrophin gene
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08-NOV-2001
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                            2607 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 2666
                                    901 CAACCICAAGCAAAIGACCAGCCCAIGGATAICCIGCAGAITAITAAITGIIIGACCAC 960
                                                                                                                                                                                                                                                        841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 900
                                                                                                                                                              721 CGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 780
                                                                                                                                                                                                             781 IGACCIGAATAATGICAGAIICICAGCIITAIAGGACIGCCAIGAAACICCGAAGACIGCA
                                                                                                                                                                                                                                                                                                                                                  961 TATTTATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTCTGCGTGGA
                                                                                                                  661 TGTCCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA
                                                                    541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG
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Example 1; Page 46-47; 71pp; English.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N'terminal or modified N'terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene operably linked to an expression control control element, in a recombinant adeno-associated virus or retroviculated virus or retroviculated to an expression useful for treating buchenne muscular dystrophy (BMD) in a mammalian subject. The present sequence is human hinge HI and rods RI and R2), 8055-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

Sequence 3999 BP; 1223 A; 907 C; 933 G; 936 T; 0 other;

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OY 1 CGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 60

Db 2268 CGACTTTCCAGCAGTTCAGAACGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 60

Db 2268 CGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 2327

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421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAA 480

2688 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCGCACGTCAA 2747 481 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 540 541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG 600 961 TATTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGA 1020 1021 TATGIGICIGAACIGGCIGCIGAATGITTATGATACGGGACGAACAGGGAGGAICCGIGT 1080 1081 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140 781 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840 841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGGCTGCATGTGATGCCTTGGACCAGCA 900 1141 ATACCITITCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGAGGCTGGGCCT 1200 1201 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260 901 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 960 3408 ATACCTITICAAGCAAGTGGCAAGTTCAACAGGATTITGTGACCAGCGCAGGCTGGGCCT 3467 1261 CAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAAGCCAGAGAT 1320 3528 CAGTAACATTCAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAAGCCACAGAT 3587 721 CGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC Human dystrophin minigene delta4173. AAD37230 standard; DNA; 4182 BP. (first entry) 21-AUG-2002 1321 C 1321 3588 C 3588 AAD37230; RESULT 7 AAD37230 pp δ ò a δy Dp δλ Dρ δ Db οy g ò qq qq ŏ Q δ Dp δλ QQ δŏ qq οy

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H and H4 domains and oysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammahlian subject. The present sequence is human dystrophin minigene delta4173 containing nucleotides I-1992 (N-terminus, hinge H1 and rods R1, R2 and R3), 8059-10227 (rods R22, R23 and R34, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2631 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAAGATACTGAGTGGGA 2690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 43-44; 71pp; English
                                                                                                                                                                                        27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                     28-APR-2000; 2000US-20077PP.
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                                                                                                                                                                                                                                                            (XIAO/) XIAO X.
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1081 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   961 TATTIAIGACCGCCIGGAGCAAGAGCACAATTIGGICAACGICCCICTCTGCGTGGA 1020
                                                                                                                                                                                                                                                                                                                                                      901 CAACCICAAGCAAAATGACCAGCCCAIGGATAICCTGCAGATTATTAATTGITIGACCAC 960
2811 CAAGGGAICCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGA 2870
                          721 CGAGACTCAAACAAGTIGCTGGGACCAICCCAAAATGACAGAGCTCTACCAGTCTTTAGC 780
                                                                                                                                                                                                                                   781 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840
                                                                                       009
                                                                                                                                                             421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAGGTGAGCCACGTCAA
                                                                                        541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG
                                                                                                                           AAD37259 standard; DNA; 4476 BP
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21-AUG-2002 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control control element. The dystrophin minigene in operable linkage with an expression control control element, in a recombinant adeno-associated virus or retrovirus is dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polya signal sequence.
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                                                             Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                               New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2535 CGACTTICCAGCAGTICAGAAGCAGAACGATGTACATAGGGCCTICAAGAGGGAATTGAA 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2595 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 2654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1321; DB 24; Length 4476;
100.0%; Pred. No. 0;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4476 BP; 1252 A; 1096 C; 1127 G; 1001 T; 0 other;
                                Adeno-associated virus vector plasmid, AAV-MCK-3510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 63-65; 71pp; English.
                                                                                                                                                                                                                                       27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                      28-APR-2000; 2000US-200777P.
                                                                                                                            Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.(
Matches 1321; Conservative
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-049342/06.
                                                                                                                                                                          WO200183695-A2.
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                                                                                                                                                                                                         08-NOV-2001.
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2835 CCAGGAACTICAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 2894
                                                    2895 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGA 2954
                                                                                                                   2955 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCACGTCAGA 3014
                                 361 CAAGGGATCCTGGCAGCCCGTGGCGATCTCCTCATTGACTCTCCAAGATCACCTCGA 420
                                                                                                                                                                                         421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGGCACGTCAA 480
                                                                                                                                                                       481 TGACCTTGGTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 540
                                                                                                                                                                                                                                                                                                                               3255 GAGACTCAAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 3314
                                                                                                                                                                                                                                            541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACGAGGACTAG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601 GCAGCIGCATGAAGCCCACAGGGACTITGGICCAGCATCTCAGCACTITCTTICCACGIC 660
                                                                                                                                                                                                                                                                                                                                                                                  661 TGTCCAGGGTCCCTGGGAGAGGCCATCTGGCCAAACAAAGTGCCCTACTATATCAACCA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 CGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3435 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 3494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 TATGTCTCAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3555 TATGTGTCTGAACTGGCTGCAGTTTTATGATACGGGACGACGAACAGGGAGGAGCGATCCGTTT 3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 CAACCICAAGCAAAAIGACCAGCCCAIGGAIAICCIGCAGAITAITAAITGITIGACCAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3615 CCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 3674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1141 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGCGGAGGCTGGGCGT 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3675 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCACACGCAGGCTGGGCCT 3734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1201 CCTICIGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260
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RESULT 9 AAD37258

2655 GCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGG 2714

121 GCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCGAGAGAG 180

ò Dp ò QQ

181 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 240

301 CCAGGAACTICAAGAGGCCACGGAIGAGCTGGACCTCAAGCTGGGCCAAGCTGAGTGAT 360

241 AAAATTGAACCTGCACTGACTGGCAGAGAAAAATAGATGAGACCCTTGAAAGACT 300

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 M-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 invention also relates to a recombinant adeno-associated virus (AAV) invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2557 CGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 2616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 120
                                                                                                   Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; ANY; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGACTITCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGAAITGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 1321; DB 24; Length 4498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4498 BP; 1251 A; 1118 C; 1123 G; 1006 T; 0 other;
                                                                            Adeno-associated virus vector plasmid, AAV-MCK-3531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 62-63; 71pp; English.
AAD37258 standard; DNA; 4498 BP.
                                                                                                                                                                                                                                                                   27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                28-APR-2000; 2000US-20077P
                                                         (first entry)
                                                                                                                                                                       Chimeric - Homo sapiens Chimeric - Unidentified
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-049342/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                        dystrophin gene -
                                                                                                                                                                                                                                                                                                                              (XIAO/) XIAO X.
                                                                                                                                                                                                                 WO200183695-A2.
                                                                                                                                                                                                                                           08-NOV-2001.
                                                            21-AUG-2002
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1141 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCAGGCTGGGCCT 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1201 CCTICTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260
                                                                                                                                                                                                                                                                                                                                                                               1081 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                      961 TATTIATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTCTGCGTGGA 1020
                                                                                                                                                                                                                                                                                                                                                          781 TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840
                                            541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG 600
481 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 540
                                                                           421 GAAAGTCAAGGCACTICGAGGAGAAATTGCGCCTCTGAAAGAAGAACGTGAGCCACGTCAA 480
               301 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 360
                                                                                                                                                                                                                                                                                                                       901 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1321 C 1321
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                    New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                   Adeno-associated virus vector plasmid, AAV-MCK-delta3849.
                                                                                                                                                                                                                                                                                                              Example 1; Page 61-62; 71pp; English.
               AAD37257 standard; DNA; 4825 BP.
                                                                                                                                                                                27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                 28-APR-2000; 2000US-200777P.
                                                21-AUG-2002 (first entry)
                                                                                                                     Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                     WPI; 2002-049342/06.
                                                                                                                                              WO200183695-A2.
                                                                                                                                                                                                                    (XIAO/) XIAO X.
                                                                                                                                                                08-NOV-2001.
                                  AAD37257;
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RESULT 10
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 invention also relates to a recombinant adeno-associated virus (AAV) ecomprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is dystrophy (BMD) in a mammalian subject. The present sequence is AAV ector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polya signal sequence.

0; Gaps 100.0%; Score 1321; DB 24; Length 4825; 100.0%; Pred. No. 0; Sequence 4825 BP; 1369 A; 1175 C; 1204 G; 1077 T; 0 other; 0; Indels Mismatches 0; Matches 1321; Conservative Similarity ò

2944 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGGG 3003 3004 GCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCTCTGAGAGAG 3063 61 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 120 121 GCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCGAGAGAG 180 1 CGACTITCCAGCAGTICAGAAGCAGAACGATGIACATAGGGCCTICAAGAGGGAATIGAA 60 q ολ qq δλ qq

181 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 240

3064 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 3123 3124 AAAATTGAACCTGCACTCCGCTGACTGGCAGAAAAATAGATGAACCCTTGAAAGACT 3183 241 AAAATTGAACCTGCACTCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACT 300 3244 CAAGGGATCCTGGCAGCCCGTCGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGA 3303 3364 TGACCTTGCTCGCCAGCTTACCACTTTGGCATTCAGCTCTCACCGTATAACCTCAGCAC 3423 301 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGCCAAGCTGAGGTGAT 360 361 CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGA 420 421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGGCGCGTCAA 480 481 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 540 541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG 600 3544 TGTCCAGGGTCCCTGGGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATCAACCA 3603 3724 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCTTTGGACCAGCA 3783 661 TGTCCAGGGTCCCTGGGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 720 721 CGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTAGC 780 961 TATITATGACCGCCTGGAGCAAAAGAACAATTTGGTCAACGTCCCTCTGCGTGGA 1020 3844 TATTTATGACCGCCTGGAGCAAGAGCACAACTTGGTCAACGTCCTCTCTGCGTGGA 3903 781 FGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840 1021 TATGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAAGGAGGATCCGTGT 1080 841 GAAGGCCCTTTGCATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 900 901 CAACCICAAGGAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 960 3904 TATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 3963 1081 CCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140 1141 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGAGGCTGGGCCT 1200 4024 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGATTTTGTGACCAGCACAGGAGGTGGGCTT 4083 4084 CCTICTGCATGATTCTATCCAAATTCCAAGATTGGGTGAAGTTGCTGAAGTTGCGTGAAGTTGCGTGAAGTTGGGGG 4143 1201 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260 4144 CAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAAGCCAGAGAT 4203 1261 CAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAAGCCAGAGAT 1320 qq δ Пþ Óγ q δλ qq δ qq δλ PP Qγ qq δ Ω Qγ Ω δy qq Op ò ŏ q Op δy ŏ O ô ŏλ qq qq δ δλ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, HI and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 120
                                                                                                                                                                                                                                                                                                                    Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                               Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4848 BP; 1405 A; 1144 C; 1180 G; 1119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 68-70; 71pp; English.
                                                                                                                                                                AAD37263 standard; DNA; 4848 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - Cytomegalovirus.
                                                                                                                                                                                                                                                      21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dystrophin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (XIAO/) XIAO X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-2001.
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                        1321 C 1321
                                                                   4204 C 4204
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                                                                                                                                   RESULT 11
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1201 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1021 TATGTGTCTGAACTGCCTGCTGAATGTTTATGATACGGGACGAACAGGAGGATCCGTGT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1141 ATACCTTTTCAAGCAAGTGGGAAGTTCAACAGATTTTGTGACCAGCGCAGGCTGGGCCT 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 CAACCICAAGGAAAATGACCAGGCCAIGGAIAICCIGCAGAITATIAAIIGITIGACCAC 960
                                                                                                                                                                                                                                                                                                     841 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGAGCTGGATGCCTTGGACCAGCA 900
                                                                                                                                                                                                                                                                         3447 rerigaagacergaacaceagarggaagericigeaggregeegregagaegaegaega 3506
                                                                                                                                                                                                                                                                                                                                                                                                        TGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840
                                                                                                                                                                                                                            721 CGAGACTCAAACATGCTGGGACCATCCCAAAATGACAGGCTCTACCAGTCTTTAGC 780
                                                                                                                                         661 IGICCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 720
                                                                         481 IGACCTTGCTCGCCAGCTTACCACTTTGGCATTCAGCTCTCACCGTATAACCTCAGCAC 540
                                                                                                                                                                                                                                                         900
                                                                                                                                                                                                                                                                                             421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAA 480
241 AAAATTGAACCTGCAGTCGCTGACTGGCAGAAAAATAGATGAGACCCTTGAAAGACT 300
                                                                                                     301 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 360
                            181 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 240
                                                                                                                                                                                                                                                         541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG
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4107 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 4166
                                    QQ
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1321 C 1321 δ

4227 C 4227 pp

RESULT 12 AAD37256

AAD37256 standard; DNA; 4966 BP. AAD37256;

21-AUG-2002 (first entry)

Adeno-associated virus vector plasmid, AAV-MCK-delta3990.

Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.

Chimeric - Unidentified, Chimeric - Homo sapiens

WO200183695-A2.

08-NOV-2001.

27-APR-2001; 2001WO-US13677.

28-APR-2000; 2000US-200777P.

(XIAO/) XIAO X.

WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a

Example 1; Page 59-60; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.

Sequence 4966 BP; 1403 A; 1216 C; 1232 G; 1115 T; 0 other;

0; Gaps Query Match
100.0%; Score 1321; DB 24; Length 4966;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0;

1 CGACTITCCAGCAGITCAGAAGCAGAACGATGIACATAGGGCCTTCAAGAGGGAATTGAA 60 g δ

61 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGGGA 120

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3085 AACTAAAGAACCIGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 3144
                                                                                 301 CCAGGAACTICAAGAGGCCACGGATGAGCTGGACCTCAAGCTGGGCCAAGCTGAGGTGAT 360
                                                                                                                                                                                              361 CAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTTCATTGACTCTCCAAGATCACCTCGA 420
                                                                                                                                                                                                                                      421 GAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAACGTGAGCCACGTCAA 480
                                                                                                                                                                                                                                                                                                                                    3865 GAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTGGGTGTGATGTGATGCCTTGGACCAGCA 3924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATTTATGACCGCCTGGAGCAAAGGACACAATTTGGTCAACGTCCCTCTGCGTGGA 1020
                                                                                                                                                                                                                                                                                                                                                                                                         661 TGTCCAGGGTCCCTGGGAGAGACCATCTCGCCAAACAAAGTGCCCTACTATATCAACCA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                 721 CGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781 IGACCIGAATAATGICAGATICTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1021 TATCTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1081 CCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1141 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGATTTTGTGACCAGCGCAGGCTGGGCT 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841 GAAGGCCCTITGCTIGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA
                                                                                                              241 AAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACT
                                                                                                                                                                                                                                                                                                                        541 TCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAG
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, Hi and H4 domains and cysteine-rich domains of dystrophin or utrophin gene, The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                      1261 CAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAATAAGCCAGAGAT 1320
                                                                                                                        1201 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260
4165 ATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCT 4224
                                                  cytomegalovirus (CMV) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 4990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid construct containing human dystrophin minigenes,
                                                                                                                                                                                                                                                                                                                                                                                                       Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4990 BP; 1439 A; 1185 C; 1208 G; 1158 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1321;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 67-68; 71pp; English.
                                                                                                                                                                                                                                                                                                      AAD37262 standard; DNA; 4990 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               adeno-associated virus; AAV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Cytomegalovirus. Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-2001.
                                                                                                                                                                                                                     4345 C 4345
                                                                                                                                                                                  1321 C 1321
                                                                                                                                                                                                                                                                                                                                            AAD37262;
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Indels

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Best Local Similarity 100.0 Matches 1321; Conservative

Similarity

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1021 TATGTCTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGAGCATCCGTGT 1080
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          361 CAAGGGAICCIGGCAGCCCGIGGGCGAICICCICATIGACTCICTCCAAGAICACCICGA 420
                                                                   121 GCCTTIGGAAGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCTGAGGAGAG 180
                                                                                                     181 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGG 240
                                                                                                                                                                        301 CCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGAT 360
                                 61 AACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCA 120
1 CGACITICCAGCAGGICAGAAGCAGAACGATGIACAIAGGGCCTICAAGAGGGAATTGAA 60
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1201 CCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGG 1260
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                                                                                         4249 CCTTCTGCATGATTCTATCCAAATTCCAAGATGGGTGAAGTTGCATGAAGTTGGGGG 4308
                                                                                                                                  4309 CAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTTGCTAATAATAAGCCAGAGAT 4368
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AAZ48567 standard; cDNA to mRNA; 4402 BP. 31-MAR-2000 (first entry) AAZ48567; AAZ48567

rod shortened dystrophin (deltaDysAx11) encoding nucleotide sequence.

Muscular dystrophy; rod domain; adeno-associated virus; AAV; dystrophin gene; truncated; ds

Homo sapiens.

JP11318467-A.

24-NOV-1999.

98JP-0142134. 08-MAY-1998;

98JP-0142134. 08-MAY-1998;

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN. (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

WPI; 2000-100771/09. P-PSDB; AAY59238. gene encoding a shortened dystrophin - useful for the treatment of muscular dystrophy

Claim 7; Page 16-17; 44pp; Japanese.

The invention provides a gene for the treatment of muscular dystrophy having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low The present sequence represents a rod shortened dystrophin encoding sequence.

Sequence 4402 BP; 1329 A; 1000 C; 1019 G; 1054 T; 0 other;

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0; Gaps
 83.7%; Score 1105.2; DB 21; Length 4402; 97.6%; Pred. No. 0:
                                       28; Indels
                    Pred. No. 0;
0; Mismatches
                           Matches 1122; Conservative
             Local Similarity
Query Match
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0

1758 TGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTAAGGAGGTCAATAC 1817 172 TGAGGAGAGGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATAC 231 ó

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232 TGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACCCT 291
                                                        292 TGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGC 351
                                                                                                                                                                                          2058 CACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGCCATTCAGCTCTCACCGTATAA 2117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         832 AAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTT 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H and H4 domains and cysteline-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to a repression control element, in a recombinant adeno-associated virus (AAV) comprising dystrophin minigene in operable linked to a repression control control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta347 containing nucleotides 1-1992 (N-terminus, hinge H1 and rods R1, R2 and R3), R3 (M49-1027) (rod R24, hinge H4 and hinge H1 and rods R1, R2 and R3), R3 (M49-1027) (rod R24, hinge H4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2112 GACTCTCTCCAAGATCACCTCGAGAAGTCAAGGCACTTCGAGGAGAATTGCGCCTCTG 2171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1992 ACAGCACAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGACCTGGACCTC 2051
                                                                                                                                                                                           Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 GACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 ATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3446 BP; 1074 A; 766 C; 787 G; 819 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 53-54; 71pp; English.
                                                                                                                                                                    Human dystrophin minigene delta3447.
                                                                           AAD37242 standard; DNA; 3446 BP
                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2000; 2000US-200777P
                                                                                                                                                                                                                                                                                                                                                        27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.6'
Matches 1040; Conservative
                                                                                                                                          21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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2898 GCCAGAGATC 2907
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                                                                                                            AAD37242;
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1178 IGIGACCAGCGCAGGCTGGGCCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTG 1237
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                                                                                                                                                                                                                                                                                                                                                                                                  998 GICAACGICCCICICIGCGIGGAFAIGICIGAACIGGCIGCIGAAIGIITATGAIACG 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2712 GTCAACGTCCTCTCTGCGTGGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACG 2771
                                                                                                                                                                                                                                                                                                                                                2232 CTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACACAGATGGAAGCTTCTGCAG 2291
                                                                                                                                                                                                                                                                                                  818 GCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCT 877
                                                                                                                                                 638 TCTCAGCACTITCTTTCCACGICTAGGGTCCCTGGGAGAGAGCCAICTCGCCAAAC 697
                                                                                                  578 GIGGCCGICGAGGACCGAGTCAGGCAGCIGCAIGAAGCCCAACAGGGACITIGGICCAGCA 637
                                                 518 CTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAG 577
458 AAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: April 25, 2003, 08:43:55
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AL556247 AL556247
BO640063 he23g04.y
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BB629984 BB629984
BB610411 BB610411
                                                                    April 25, 2003, 07:58:12 ; Search time 1246 Seconds (without alignments) 17170.339 Million cell updates/sec
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GenCore version 5.1.4_-p5_-4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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1321
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                                              OM nucleic - nucleic search, using sw model
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Un-normalized, unamplified): hd/he
                 cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Fmail: fliangelifetech.com URL:

http://tulllength.invitrogen.com"
                                                                                                                                                                                                                                                                 ó;
enriched, double-stranded cDNA was digested with Not I and
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 620)
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Homo sapiens cDNA clone he23g04 5', mKNA sequence.
B0640063.1 GI:21764522
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728 GATC 731

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human.

ORGANISM

REFERENCE

DEFINITION

RESULT 2 BQ640063 ACCESSION

KEYWORDS

VERSION

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/note—"Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTACTTCTACATCCGACGGCCCCC(T)]. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), (2002) In press
Contact: Wistow G
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44.9%; Score 593; DB 14; Length 62
Best Local Similarity 100.0%; Pred. No. 4.4e-167;
Matches 593; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                       Section on Molecular Structure and Function National Eye Institute
                                                                                                                                                                                                                                                        6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                   Email: graeme@helix.nih.gov
Plate: 23 row: g column: 04
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/lab_host="EMDH10B"
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S. Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itch, M., Izawa, M., Koyawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koyawa, T., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, H., Saaico, R., Sano, H., Sasai, D., Schrind, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamanura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="hippocampus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. 2135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                      Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                          and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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/db_xref="MGDN0X1:1905833"
/db_xref="taxon:10090"
/clone="290010C03"
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124. .900
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                                                                                                                                                                                                                                                                                                                                                                                                                       HTC 19-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK013510.1 GI:12850899
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male hippocampus cDNA to mRNA, clone_lib:RKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Nazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapilary sequencer Gennat Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900010C03:dystrophin, muscular dystrophy, full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                        ATGATICTATCCAAATICCAAGACAGTIGGGIGAAGTIGCATCCTTIGGGGGCCAGTAACA 1268
1149 TCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGC 1208
                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.l column: 08
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96.5%; Pred. No. 1.7e-150;
tive 0; Mismatches 18;
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                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4822807"
                                                                                                                                                                                                                      /clone_lib="NIH_MGC_97"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652 bp
                                                                                                 High quality sequence stop: 767.

Location/Qualifiers
1. .770
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Matches 572; Conserva
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602690430F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4822807 5',
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 770)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTATITATGACCGCCTGGAGCAAGAGCACAATITGGTCAACGTCCCTCTCTGCGT 1017
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                 264 CCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCCTGGACCA 323
                                                                                                                                                                                                                                                                                                                                                                                                        324 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATAATTAACTGTTTGAC 383
                                                                                                                             718 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 777
                                                                                                                                                                 144 CCACGAGACCCAAACCACTTGTTGGGACCACCACAAAATGACAGAGCTCTACCAGTCTTT 203
                                                                                                                                                                                                          778 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 837
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                                                   DB 11; Length 2135;
                                                                                        Indels
                                                                                          39;
                                                   Score 540.6; DB 11
Pred. No. 6.9e-151;
                                                                                        0; Mismatches
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                                                   40.9%;
93.5%;
                                                 Query Match
Best Local Similarity 93.5'
Matches 564; Conservative
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BG719710
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DEFINITION

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ACCESSION

VERSION KEYWORDS

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AUTHORS REFERENCE

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EST 31-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1016 GIGGAIAIGIGICIGAACIGGCIGCIGAAIGITIAIGAIACGGGACGAACAGGGAGGAIC 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 ACCACTATITATGACCGCCTGGAGCAAGAGCACAACTATTGGTCAACGTCCCTCTGC 449
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                                                                                                                                                                                                                                                                                                                         718 CCACGAGACTCCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 777
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VERSION KEYWORDS

SOURCE

REFERENCE AUTHORS

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1711 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kondo, H., Koya, S., Matsuyama, T., Ito, M., Kawai, J., Kondo, H., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, K., Sano, H., Sasaki, Tagami, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M., and Hayashi, F., Takeda, Y., Tanaka, T., Toya, T., Unpublished (2001)
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 612)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-resigns.riken.go.jp,
UKL:http://genome.go.go.
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trotte="Site_1: Sal; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGAGACCCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="9930028B14"
/clone_lib="RIKEN full-length enriched, adult female
BB629984 RIKEN full-length enriched, adult female vagina Musmusculus CDNA clone 9930028B14 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="vagina"
/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                           BB629984.1 GI:15399733
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JOURNAL
COMMENT
                                                                         ACCESSION
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PEATURES

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1 (bases 1 to 704)
Arakava,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 26-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB610411 RIKEN full-length enriched, 10 day old male pancreas Musmusculus cDNA clone 1810074E05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1017
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                                                                                                                                                                                                                                                                                                                                                                                                        898 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 957
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                                                                                                                                                                                                                                        1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.1%; Score 502.8; DB 10; Length 652; 92.6%; Pred. No. 7e-140; Live 0; Mismatches 42; Indels 1;
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Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.P., Shibata,Y., Hayatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapled discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fuliwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Ratahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                    Contact: Yoshihidé Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nayasnızakı,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagani,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T. Muramatsu,M. and Hayashiaki,Y..
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/clone="1810074E05"
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FEATURES

37.2%; Score 491.6; DB 10; Length 704;

Query Match

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AI196693 B54 bp mRNA linear EST 14-OCT-1998 ui53el0.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1886154 5' similar to gb:M18533 DYSTROPHIN (HUMAN); gb:M68859 Mouse dystrophin mRNA, exons 1-7 and complete cds (MOUSE);, mRNA
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                         718 CCACGAGACTCCAAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 777
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                     Indels
  Pred. No. 1.8e-136;
                       0; Mismatches
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Contact: Marra M/Mouse EST Project
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93.08;
      Best Local Similarity 93.0%
Matches 515; Conservative
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674 GGGGCAGTAACATTGAGCCGAGTGTCAGGAGCTGCTTCCACTTT 717
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                                                                                                                                                                                                                                                                       Mas primed with an oligo(dT) primer (ATGTGGCCTTTTTTTTTTTTTT], double-stranded CDNA was ligated to a Draili adaptor [TGTTGGCCTACTGG], digested and cloned into distinct Draili sites of the pMEB8-FL3 be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                        Constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGGTCTAAAAGCTGGG and 3' end primer CGACCTGCAGCTCGACCCAAC. 3 others
                                                                                                                                                                                                                                             /note="Organ: liver; Vector: PME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:970478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                958 CACTAITIAIGACCGCCIGGAGCAAGAGCACAATITIGGICAACGICCCTCTCTGGGT 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018 GGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCC- 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1077 GIGICCIGICITITAAAACIGGCAICAITICCCIGIGIAAAGCACAITIGGAAGACAAGI 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      718 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1197 GCCICCTICIGCAIGAITCIAICCAAAITCCAAGACAGITGGGIGAAGIIGCAICCIIIG 1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 838 GCAGAAGGCCCTTTGCTTGGAICTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  898 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   555 ACAGATACCCTTTCAAGCAAGTGGCAAGTTCAACTGGCTCNTGTGACCAGCGTANGCTGC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615 GTCTTCTTCTGCATGAATCTATTCACATCCCAAGACAGGTTGGTGAAAGTGCTTCCTTT- 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.3%; Score 479.6; DB 9; Length 854; 90.9%; Pred. No. 8.4e-133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1257 GGGGCAGTAACATTGAGCCAAGTGTCCGGAGCTGCTTCCAATTT 1300
                                                                                                                                                                             /clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                               /organism="Mus musculus"
                                           Seq primer: custom primer used
High quality sequence stop: 460.
Location/Qualifiers
                                                                                                                                            /db_xref="taxon:10090"
                                                                                                                                                                 /clone="IMAGE:1886154"
                                                                                                                                                                                                            /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                             /strain="C57BL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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BF182065
601804604F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4035505 5',
                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 898)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         955 GACCACTATTTATGACCGCCTGGAGCAAGAGCACAA-CAATTTGGTCAACGTCCCTCTT 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 CCACGAGACCCAAACCACTTGTTGGGACCACCCCAAAATGACAGACTCTACCAGTCTTT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       838 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCA-TGTGATGCCTTGGACC 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     897 AGCACAACCTCAAGCAAAATGA-CCAGCCCATGGATATCCTGCAGATTATTAA-TTGTTT 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:4035505"
/clone=lib="NOI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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High quality sequence start: 3
High quality sequence stop: 675.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

    .898
    /organism="Mus musculus"

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                                                                                                   BF182065.1 GI:11060207
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.6e-112;
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                                                                                                                                                                                          /organism="Mus musculus"/db_xref="taxon:10090"
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                              /clone="E330026B12"
                                                                                                                                                                                                                                                                                                             adult female ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.1%;
93.3%;
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                                                                                                            e mouse tissues.
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Konno, H., Pukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Komputer-based methods for the mouse full-length CDNA computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fikuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mandalida; Luciation, Nocentra, Control, Mandalida; Luciation, Nocentra, Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kouno, H., Kouda, M., Koyas, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., M., Koyas, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-resigns.riken.go.jp,

Banalis genome-resigns.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

Carninci,P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Toaqawa,M., Ohara,E.,

Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB666688 RIKEN full-length enriched, 2 days pregnant adult female ovary mus musculus cDNA clone E330026B12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Tokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                    1133 AAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGG 1192
                                                                                                                                                                                                                                                                                                                                                                                    1193 CIGGGCCICCTICIGCATGATICTAICCAAATICCAAGACAGTIGGGIGAAGTIGCAICC 1252
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                                                                                                                                              1073 ATCCGTGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGAC 1132
                           1014 GCGTGG-ATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGG 1072
                                                                                                                                                                                   667 TGTGGGGGCAGGAACATTGAGCCGAGTGCTCAATTTTGCCAAGTAATAG 726
                                                              BB666688.1 GI:16500321
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JOURNAL
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ACCESSION

KEYWORDS

VERSION

RESULT 9 BB666688

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COMMENT

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EST 12-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                           /tissue_type="ovary"
/dev_stage="2 days pregnant adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was cleaved with BamHI and XhoI. Vector: a modified pbluescript KS(+) after bulk excision from Lambda FLC I." 161 c 142 g 150 t
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/clone_lib="RIKEN full-length enriched, 2 days pregnant
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AL641565 XGC-neurula Silurana tropicalis cDNA clone TNeu012d20 5'
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ambhlbia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
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TROPICALIS_SEQUENCE_ID: TNeu012d20.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu012d20"
                                                                                                                                                                                                                                                                                               Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="XGC-neurula"
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                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Aaron M. Zorn.
Location/Qualifiers
                                                         AL641565.1 GI:16793690
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                                                                                            western clawed frog.
                                                                                                                Silurana tropicalis
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                     mRNA sequence.
AL641565
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 423)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie WashU-Merck EST project 1997
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                                                                                                                                     AA460476 423 bp mRNA linear EST 09-JUN-1
zx61e10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:795978 5' similar to 9b:M18533 DYSTROPHIN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 287.
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Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xrof="CDB:6039697"
/db_xrof="taxon:9606"
/clone="InAGE:795978"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH108"
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1198 CCTCCTTCTGCATGATTCTATCCAAATTCC 1227
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                     655 CCTGCTTTTACATGATGCAATTCC 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
                                                                                                                                                                                                                                          AA460476.1 GI:2185222
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233 GCAAAAGGCCTTGTGCTTGGATTTGCTAAGGCTGTCTGCAGCTTGTGAAGCCTTGGACCA 292
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/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2002 Unpublished (2001)
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                                                     267 CACTATTTATGACCGCCTGGAGGAAGAGCACAACAATTTGGTCAACGTCCCTCTGGGT 326
                                                                                                                                                                                                              1; Gaps
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Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu143c03.plcSP6
Sequencing primer: PlCSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
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28.8%; Score 380.4; DB 9; Length 633;
Best Local Similarity 84.3%; Pred. No. 5.3e-103;
Matches 440; Conservative 0; Mismatches 81; Indels 1.
                                                                                                                                                                                                                                                                        1077 GIGICCIGICTITIAAAACTGGCATCATITCCCTGIG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                             387 GTGTCCTGTCTTTTAAAACCGGCATCATTTCCCTGTG 423
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/clone="TNeu143c03"
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AL796733
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i (bases 1 to 665).
Clark, M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S.L., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, S., Hiller, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE201973 665 bp mRNA linear EST 30-AUG-2000 fl03h06.xl Zebrafish Research Genetics C32 fin Danio rerio cDNA 3' similar to TR:Q02295 Q02295 MAJOR DUCHENNE MUSCULAR DYSTROPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pT7T3D-Pac with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared from zebrafish(C32) fin, and was then primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="GeneHogs (HS996, a phage-resistant isolate of
                                                                                                             958 CACTATITATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGT 1017
                                                                                                                                                                                                                                  1018 GGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 1077
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Frax: 314 286 1810
Email: 2brafish@vatson.wustl.edu
cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone lib="zebrafish Research Genetics C32 fin"
/tissue_type="Fin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1198 CCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGG 1239
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Unpublished (1998)
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Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is non-normalized. Library was constructed by Ming Wu NOTE: Clones from this library are only available thru Research Genetics (www.resgen.com)."

174 c 176 g 157 t 2 others
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oligo(dT) primer. Double-stranded cDNA was ligated to
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Silurana
1 (bases 1 to 608)
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                                                                                                                                                                                                                                                                                                                                     800 ITCTCAGCTIATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGAT 859
                                                                                                                                                                                                                                                                                860 CTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGAC 919
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                                                                                                                                                                        f Match 27.1%; Score 358.2; DB 10; Length Local Similarity 75.9%; Pred. No. 2.7e-96; nes 441; Conservative 0; Mismatches 140; Indels
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/lab_host="Escherichia coli XLI-blue"
/note="vector: pCSI07; Site_1: ECORI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. ECORI-NotI cut cDNA was then ligated
into pCSI07 with ECORI at the 5' end and NotI at the 3'
end."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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This sequence is from a Xenopus Gene Collection (XGC) library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 330; DB 9; Length 608; 85.0%; Pred. No. 7.9e-88; tive 0; Mismatches 65; Indels
                Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas054h08.plcSP6
Sequencing primer: PlCSP6
                                                                                                                                                                         /organism="Silurana tropicalis"
Hinxton, Cambridgeshire, CB10 1SA, UK
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                                                                                                                                                                                                                /clone="TGas054h08"
/clone_lib="XGC-gastrula"
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                                                                                                                       Zorn.
                                                                                                                 constructed by Aaron M. Zorn.
Location/Qualifiers
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(bases 1 to 532)

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CDNA was
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                             Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-refmail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="inAGE:1550362"
/scone=lib="Soares mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
                                                                                                                                                                                                                    Red primer: -40RP from Gibco
High quality sequence stop: 449.
Location/Qualifiers
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Job time : 1257 secs

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Sequence 5, Appli
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                                                                                                                                   1 cgactttccagcagttcaga......ttaataataataagccagagatc 1321
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Sequence 13, 7
Sequence 370,
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                                                                  April 25, 2003, 08:10:12; Search time 30.0867 Seconds
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptcdata/1/ina/5A_COMB.seq:*
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/cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/1/ina/FCTUS_COMB.seq:*
/cgn2_6/ptcdata/1/ina/FCTUS_COMB.seq:*
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US-08-676-967-5
US-09-671-950-3
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US-09-671-950-3
US-09-671-950-3
US-09-671-950-7
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US-08-874-116-1
US-08-877-116-1
US-08-877-116-3
US-08-747-116-3
US-08-747-116-3
US-08-747-116-3
US-09-153-804-2
US-08-728-323A-1
US-08-728-566-1
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-425-069-3
US-08-317-844B-3
                                                                                                             US-09-845-416-10_COPY_1800_3120
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US-08-668-128B-7
                                                                                                                                                                                           441362 segs, 153338381 residues
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                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 5000
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Sequence 7, Appli Sequence 116, App Sequence 14, Appl Sequence 368, Appl Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 6, Appli	PER SILK AND A TRANSFORMED CELL AND PRODUCTS THEREOF
2085 2 US-08-905-445-7 3079 4 US-09-643-597-116 2470 1 US-08-311-363-14 941 4 US-08-961-527-368 1453 4 US-09-153-804-7 1875 2 US-09-153-804-7 1875 4 US-09-153-804-7 1875 4 US-09-153-14 276 4 US-09-222-575-80 2610 2 US-09-212-771-1 2610 3 US-08-961-527-363-2610 2610 3 US-08-961-527-363-3 2610 3 US-08-961-58-1 1626 3 US-08-96-1 1626 3 US-08-96-1 1639 3 US-08-895-601-2 1443 3 US-08-895-818-3 1599 3 US-08-853-733B-1 1603 3 US-08-853-733B-1	RESULT 1 US-08-425-069-3 Sequence 3, Application US/08425069 Patent No. 5728810 GENERAL INFORMATION: APPLICANT: Lewis, Randolph V. APPLICANT: NUMBER: 28,977 REFERENCE CHARACTERISTICS: Lewis, Randolph V. APPLICANT: NUMBER: 28,977 REFERENCE CHARACTERISTICS: Lewis, Randolph V. APPLICANT: Linear APPLICANT: Linear APPLICANT: Linear APPLICANT: Condolph V. APPLICANT: Linear APPLICANT: Linear APPLICANT: Condolph V. APPLICANT: Linear APPRICATE: Dobe Pairs TURE FRANCE: DOB APPLICANT: Condolph V. APPLICANT: Condolph V. APPLICANT: Condolph V. APPLICANT: Condolph V. APPLICANT: Linear APPRICATE: Painear APPRICATE: Condolph V. APPLICANT:
28 32.8 2.5 30.0 32.4 2.5 30.0 32.4 2.5 30.0 32.4 2.5 30.0 32.2 2.4 24.24 24.24 3.5 30.8 2.3 15.5 2.4 18.2 2.4	A PESULT 1 15-08-125-069-3 1 Sequence 3' Application US/08425069 2 EACENT ON 5728810 2 GENERAL INFORMATION: APPLICANT: Lewis, Randolph V. APPLICANT: Lewis, Randolph V. APPLICANT: Hinman, Michael B. TITLE OF INVENTION: PROTEIN, A FITTLE OF INVENTION: PROTEIN, A FITTLE OF INVENTION: CONTAINING TYPE: Fals Church Stewart, Kolstein Street: 301 No. 5728810th Wash CITY: Fals Church Stewart, Kolstein Street: 1301 No. 5728810th Wash CITY: Fals Church Stewart, Kolstein Street: 1301 No. 5728810th Wash CITY: Fals Church Stewart, Wolstein Street: 1301 No. 5728810th Wash CITY: Fals Church Stewart: U.S.A. 2 ID: 22046 COMPUTER READABLE FORM: WEDIUM TYPE: Ploppy disk COMPUTER: Datentin Release #1. 2 ID: 2004 The Compatible OPERATING SYSTEM: PC-DOS/MS-
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APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            971 TAGGAGGTTATGGACCAGGACAACAAGGTCCAGGAGGATATGGACCAGGACAACAAGGTC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 CAAGAGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCC 370
                                                                                                                                                                                                                                                                                                                                                                                  911 GACCATCTGGAGCAGCAGCAGCAGCAGCGGCGCAGCAGGACCTGGACAACAAGAT 970
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                                                                                                                                                                                                                                                                                                   851 GACCTGGAGGATATGGCCCTGGACAACAAGGACCCGGAGGATATGGACCAGGACAAAAG 910
                                                                                                                                                                                                                                                                                                                                            191 GTCACTCGGCTTCTACGAAAGCAGGCTGAGGGCTCAATACTGAGTGGGAAAAATTGAAC 250
                                                                                                                                                                       71 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA 130
                                                                                                                                                                                                                                                          731 GCAGTGCAGCTGCAGCAGCAGCAGCACCTGGACAACAAGAAGGACCCGGAGGATATGGAC 790
                                                                                                                                                                                                                791 CAGGACAACAAGGACCATCTGGACCCGGTAGTGCCGCTGCAGCAGCAGCCGCCGCAGCAG 850
                                                                                   11 GCAGITCAGAAGCAGAACGAIGTACAIAGGGCCIICAAGAGGGAAITGAAAACTAAAGAA 70
                                               Gaps
                                               0
2.9%; Score 38.6; DB 1; Length 1995; 44.0%; Pred. No. 0.034; tive 0; Mismatches 209; Indels 0.
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FILING COMMER: US/NR/317 0/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: Birch, Stewart, Kolasch & Birch
: 301 No. 5989894th Washington Street
Falls Church
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04-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995 base pairs
                                    Best Local Similarity 44.08
Matches 164; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1091 AAGGACCAGGAGG 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 TGGCAGCCCGTGG 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 GTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAAC 250
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                                                                                                                                                                                                                                                                                                                                                                                 71 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA 130
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                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                        Match 2.9%; Score 38.6; DB 2; Length 1995; Local Similarity 44.0%; Pred. No. 0.034; les 164; Conservative 0; Mismatches 209; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Science & Technology Law Group 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLINS, KATHLEEN
VENTION: Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08676967
Patent No. 5747317
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                          Matches 164; Conservative
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                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
TYPE: nucleic acid
                                                    MOLECULE TYPE: CDNA HYDOTHETICAL: NO
                                                                                                                                                                           1..1785
                                       linear
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                                                                                               IMMEDIATE SOURCE:
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US-08-676-967-5/c
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                                                                               HYPOTHETICAL:
                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                               US-08-317-844B-3
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1731 GAACTCCACGATGGGGCGCTTCAGGGGGCCGAAGATCTCGGGGTTGTTGTTGATCAGGCG 1672
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                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                              2.6%; Score 34.6; DB 1; Length 2277; 47.5%; Pred. No. 0.73; tive 0; Mismatches 114; Indels 0.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1611 GCCCTTCATGTTGCCGTGCACGCCCTTCAGGTCGCGC 1575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEPHONE: (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/676,974
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JS-08-676-974-5/c
Sequence 5, Application US/08676974
...
Datent No. 5770422
TELECOMMUNICATION INFORMATION:
              (415)343-4341
(415)343-4342
(415)360 ID NO: 5:
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TITLE OF INVENTION: Human Tel
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                          LENGTH: 2277 base pairs
                                  TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            Best Local Similarity 47.59
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                              nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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MOLECULE TYPE: CDNA
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MOLECULE TYPE: CDNA
S-08-676-974-5
                                                                                                                              STRANDEDNESS:
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                    TELEPHONE:
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                                                                                308 CITCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGA 367
                                                                                                                                                            368 TCCTGGCAGCCCGTGGGCGATCTCCTTCATTGACTCTCCCAAGATCACCTCGAGAAGTC 427
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                                                         0; Gaps
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Query Match
2.6%: Score 34.6; DB 1; Length 2277;
Best Local Similarity 47.5%: Pred. No. 0.73;
Matches 103; Conservative 0; Mismatches 114; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.6%; Score 34.6; DB 2; Length 2277; 47.5%; Pred. No. 0.73; Live 0; Mismatches 114; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/098,487
                                                                                                                                                                                                                                                                                                                                           1611 GCCCTTCATGTTGCCGTGCACGCCCTTCAGGTCGCGC 1575
                                                                                                                                                                                                                                                                                                                  488 GCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCAC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Science & Technology Law Group 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: COLLINS, Kathleen
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-098-487-5/C
US-09-098-487-5/C
S-09-098-487-5/C
Patent No. 5917025
GENERAL INFORMATION:
APPLICANT: COLLINS, Kathleen
Telon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,627
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TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2277 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 268 bus.
CITY: San Francisco
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MEDIUM TYPE: Floppy
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EDNESS: double
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; MOLECULE TYPE: CDNA
US-09-098-487-5
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ORGANISM: Haematobia irritans
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LENGTH: 1047
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US-09-671-950-7
                                                              NAME/KEY: CDS
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US-09-671-950-5
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TYPE: DNA
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APPLICANT: Rubin, Eric
APPLICANT: Robertson, Hugh
TITLE OF INVENTION: Hyperactive Mutants of Himarl Transposase and Methods
TITLE OF INVENTION: For Using the Same
TITLE OF INVENTION: For Using the Same
                                                                                                                                                                                                                                         Sequence 1, Application US/09671950
Sequence 1, Application US/09671950
Patent No. 636830
GENERAL INFORMATION:
APPLICANT: Lampe, David
APPLICANT: Akerley, Brian
APPLICANT: Rubin, Eric
APPLICANT: Robertson, Hugh
TITLE OF INVENTION: Hyperactive Mutants of Himarl Transposase and Methods
TITLE OF INVENTION: for Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 GGAAATCAACAATAATTGATTGGTATGCAAATTCAAGCGTGGTGAAATGAGCACGGAGG 169
                                1671 CAGGGCCTTCAGGGCGTGCTCGTGCAACGCGAAGGCGTAGCCCAGGCTCTG 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 GAAAGCAGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACT 266
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    428 AAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTT 487
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2.6%; Score 34.4; DB 4; Length 1047;
Best Local Similarity 51.3%; Pred. No. 0.52;
Matches 80; Conservative 0; Mismatches 76; Indels 0
                                                                                                                        1611 GCCCTTCATGTTGCCGTGCACGCCCTTCAGGTCGCGC 1575
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                                                                                            488 GCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCAC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APLICATION NUMBER: US/09/671,950
CURRENT APPLICATION NUMBER: US/09/671,950
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/157,680
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/671,950 CURRENT FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: 60/157,680 PRIOR FILING DATE: 1999-10-01 NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin Ver: 2.0
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Akerley, Brian
Rubin, Eric
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US-09-671-950-1
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GENERAL INFORMATION:
APPLICANT: Lampe, David
APPLICANT: Rubin, Eric
APPLICANT: Rubin, Eric
APPLICANT: Robertson, Hugh
TITLE OF INVENTION: Hyperactive Mutants of Himarl Transposase and Methods
TITLE OF INVENTION: Gor Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 GGCAGAGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATG 326
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                                                                                                                                                                                              267 GGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATG 326
                                                                                                                                                                                                                                                                                                           110 GGAAATCAACAATAATTGATTGGTATGCAAAATTCAAGCGTGGTGAAATGAGCACGGAGG 169
                                                                                                               Gaps
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                                                       Query Match
2.6%; Score 34.4; DB 4; Length 1047;
Best Local Similarity 51.3%; Pred. No. 0.52;
Matches 80; Conservative 0; Mismatches 76; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/671,950 CURRENT APPLICATION NUMBER: US/09/671,950 PRIOR APPLICATION NUMBER: 60/157,680 PRIOR PILING DATE: 1999-10-01 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/09671950
; Patent No. 6368830
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09671950 Patent No. 6368830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Haematobia irritans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.3%
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , NAME/KEY: CDS
; LOCATION: (1)..(1044)
US-09-671-950-5
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; LOCATION: (1)..(1044)
US-09-671-950-3
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Lampe, David

APPLICANT:

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RESULT 11
US-09-671-950-11
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US-09-671-950-13
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APPLICANT: Akerley, Brian
APPLICANT: Rubin, Eric
APPLICANT: Robertson, Hugh
TITLE OF INVENTION: Hyperactive Mutants of Himarl Transposase and Methods
FILE REFERENCE: 79-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lampe, David
APPLICANT: Akerley, Brian
APPLICANT: Rubin, Eric
APPLICANT: Rubin, Eric
APPLICANT: Robertson, Hugh
TITLE OF INVENTION: Hyperactive Mutants of Himarl Transposase and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                          207 GAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACT 266
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2.6%; Score 34.4; DB 4; Length 1047;
Best Local Similarity 51.3%; Pred. No. 0.52;
Matches 80; Conservative 0; Mismatches 76; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                              2.6%; Score 34.4; DB 4; Length 1047;
51.3%; Pred. No. 0.52;
tive 0; Mismatches 76; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/671,950
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/157,680
PRIOR FILING DATE: 1999-10-01
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CURRENT APPLICATION NUMBER: US/09/671,950
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/157,680
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09671950 Patent No. 6368830
                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Haematobia irritans
                                                                                                                                                                    NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Haematobia irritans
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 51.30 hes 80; Conservative
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US-09-671-950-7
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; LOCATION: (1)..(1044)
US-09-671-950-9
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                                                                                                                                                                                                        SEQ ID NO 7
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SEQ ID NO 9
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APPLICANT: Akerley, Brian
APPLICANT: Robertson, Hugh
TITLE OF INVENTION: Hyperactive Mutants of Himarl Transposase and Methods
FILE REFERENCE: 79-99
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APPLICANT: Lampe, David
APPLICANT: Rubin, Eric
APPLICANT: Rubin, Eric
APPLICANT: Robertson, Hugh
TITLE OF INVENTION: Hyperactive Mutants of Himarl Transposase and Methods
267 GGCAGAGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATG 326
                                       110 GGAAATCAACAATAATTGATTGGTATGCAAAATTCAAGCGTGGTGAAATGAGCACGGAGG 169
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51.3%; Pred. No. 0.52;
ive 0; Mismatches 76; Indels 0;
                                                                                327 AGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCA 362
                                                                                                                   170 ACGGTGAACGCAGTGGACGCCCGAAAGAGGTGGTTA 205
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CURRENT APPLICATION NUMBER: US/09/671,950
CURRENT PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/157,680
PRIOR FILING DATE: 1999-10-01
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CURRENT APPLICATION NUMBER: US/09/671,950
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/157,680
PRIOR FILING DATE: 1999-10-01
                                                                                                                                                                                                                            ; Sequence 11, Application US/09671950 ; Patent No. 6368830
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; Patent No. 6368830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Haematobia irritans
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SOFTWARE: Patentin Ver. 2.0
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SOFTWARE: Patentin Ver. 2.0
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US-09-671-950-11
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tes 80; Conserv
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US-08-874-138-1
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                         50 GAAAAATACAGTGGAAGCAAAACTTGGCTTGATAATGAGTTTCCGGACTCTGCCCCAG 109
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2.6%; Score 34.2; DB 4; Length 750;
Best Local Similarity 60.0%; Pred. No. 0.49;
Matches 57; Conservative 0; Mismatches 38; Indels
                                                                                                                                      Ouery Match

2.6%; Score 34.4; DB 4; Length 1047;
Best Local Similarity 51.3%; Pred. No. 0.52;
Matches 80; Conservative 0; Mismatches 76; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                327 AGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCA 362
                                                                                                                                                                                                                                                                                                                                                                                                                      170 ACGGTGAACGCAGTGGACGCCCGAAAGAGGTGGTTA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 370, Application US/08961527 Patent No. 6420135 GENERAL INFORMATION:
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 370:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PBS
TELECOMMUNICATION INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                   ORGANISM: Haematobia irritans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                   ; NAME/KEY: CDS
; LOCATION: (1)..(1044)
US-09-671-950-13
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US-08-961-527-370
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US-08-961-527-370
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LENGTH: 1047
                         TYPE: DNA
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1036 GCTGCTGARGTTTAICATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTTAAAAC 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 GGATATGGAGCAGATAAAAGAGATCTACGACTCGGTCTTAAGGGATTCCAGTCAGAAATT 582
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38 CAGCCTCAGCAAGTACTAGTGCATCAGCATCAGCATCAGCGTGCATCAGCCTCAGCAA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Match 2.6%; Score 34.2; DB 4; Length 1620; Local Similarity 50.9%; Pred. No. 0.8; 78; Indels 0; Aismatches 78; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1096 TGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAA 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                              APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                              179 AGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCA 213
                                                                   98 GTATCTCAGCGTCTGAATCGGCATCAACGAGTGCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMBER: US/08/858,207A 09-MAY-1997
                                                                                                                                                                                     Sequence 56, Application US/08858207A Sequence 56, Application US/08858207A Patent No. 6348328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14 MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P5C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38,891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gimmi, Edward R
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                      Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19406-0939
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US-08-858-207A-56
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Sequence 1, Application US/08874138

Sequence 1, Application US/08874138

GENERAL INFORMATION:

APPLICANT #1115, Nicola

TITLE OF INVERFION:

NUMBER OF SEQUENCES:

GORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

STREET: 997 Lenox Drive, Building 3, Suite 210

STREET: 997 Lenox Drive, Building 3, Suite 210

COUNTRY: USA

CONPUTER: NJ

COMPUTER: NSADABLE FORM:

MEDIUM TYPE: Diskette

OCOMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: ReatSEQ for Windows Version 2.0

APPLICATION NUMBER: US/08/874,138

FLING DATE:

ATTORNEY AGENT INFORMATION:

REGISTRATION NUMBER: 29,135

PRIOR APPLICATION NUMBER: 29,135

PRIOR APPLICATION NUMBER: CANDON: Allen

REGISTRATION NUMBER: 29,135

FLING DATE:

ATTORNEY AGENT INFORMATION:

TELEPHONE: 609-520-3214

TELEPHONE: 609-520-3214

TELEPHONE: 609-520-3214

TELEPHONE: GOS-520-3214

TELEPH
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Search completed: April 25, 2003, 17:43:52 Job time : 43.0867 secs

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(without alignments)
16376.941 Million cell updates/sec
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Sequence 10, Appl
Sequence 466, App
Sequence 466, App
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Sequence 442, App
Sequence 30349, A
Sequence 3955, Ap
Sequence 2757, Ap
Sequence 2757, Ap
Sequence 2758, Ap
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Sequence 157, App
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Sequence 1, Appli
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Sequence 8059, Ap
Sequence 14430, A
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                                                                            April 25, 2003, 17:39:49 ; Search time 87.7709 Seconds
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'Ggn2_6/Ptcdata/1/pubpna/USO7_PUBCOMB.seq:*
'Ggn2_6/Ptcdata/1/pubpna/USO6_BUBW_PUB.seq:*
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'Ggn2_6/Ptcdata/1/pubpna/USO8_NEW_PUB.seq:*
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'Ggn2_6/Ptcdata/1/pubpna/USO0_NEW_PUB.seq:*
'Ggn2_6/Ptcdata/1/pubpna/USO0_NEW_PUB.seq:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-918-995-30349
US-09-738-626-2757
US-09-738-626-2758
US-10-184-644-348
US-10-184-634-348
US-10-184-634-348
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US-09-960-352-8059
US-09-960-352-14430
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US-09-747-116-1
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Listing first 45 summaries
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Match Length DB ID
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Maximum DB seq length: 5000
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Sequence 5218, Ap
Sequence 575, App
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Sequence 116, App
Sequence 116, App
Sequence 34, App
Sequence 9375, Ap
Sequence 21329, Ap
Sequence 21329, A
Sequence 29, Appl
Sequence 70, Appl
Sequence 64, Appl
Sequence 649, Appl
Sequence 143, Appl
Sequence 143, Appl
Sequence 143, Appl
Sequence 143, Appl
Sequence 154, Appl
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Sequence 1352, Ap
Sequence 2427, Ap
Sequence 10622, A
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Sequence 458, App
Sequence 24845, A
Sequence 348, App
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51.9%; Pred. No. 7.2e-08;
tive 0; Mismatches 113; Indels C
                                                                                                                                                                                                                                                                                                                                                                             Sequence 241084, Application US/09918995
Fublication No. U0220030073623A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
FRIOR APPLICATION NUMBER: US/09/235,076
FRIOR FILING DATE: 1999-01-20
                                                                               US-10-184-644-458
US-10-184-644-458
US-09-918-995-24845
US-09-764-868-348
0 US-09-755-705-116
0 US-09-850-716A-116
    0 US-09-960-352-5218
0 US-09-966-708-575
0 US-09-925-301-536
0 US-09-815-242-7731
US-09-954-531-1352
                                                           US-09-880-107-2427
US-09-960-352-10622
   10 US-09-960-352-5218

10 US-09-969-708-575

10 US-09-925-301-536

10 US-09-915-31-1352

10 US-09-964-31-1352

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10 US-09-918-918-918

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10 US-09-976-950-975
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US-10-102-806-45
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24084
LENGTH: 449
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24084
   Conservative
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  Best Local Similarity
Matches 122; Conserv
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                                                                   TYPE: DNA
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US-10-184-644-442
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APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Mood, William I.
APPLICANT: TILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPRENCE: P3430R1C227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1148 TTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGCGGGGGTGGGCTCCTTCTG 1207
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          Query Match

4.1%; Score 54.2; DB 10; Length 2247;
Best Local Similarity 51.9%; Pred. No. 2e-07;
Matches 122; Conservative 0; Mismatches 113; Indels 0;
                                                                                                                                                                                         APPLICANT: Benson, Darin R.
APPLICANT: Mohamath, Raodoh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION UNBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 442
LENGTH: 440
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/960,253
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
SOFTWARE: EastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 2247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 442, Application US/10184644
Publication No. US20030044930Al
                                                                                                                                      Sequence 157, Application US/09960253
Patent No. US20020123619A1
GENERAL INFORMATION:
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 210121.556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens US-09-960-253-157
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                                                                                                                                                                                                                                                                                                                                                                                                                                          788 AATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCC 847
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                                                                                                                                                                                          369 T...CYKHK..NHRCDWCY.WC.YYCASNKW...K.YN.A..WC.HTB.A..SB.MCMMR 310
                                                                                                                                                                                                                                                668 GGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACT 727
                                                                                                                                                                                                                                                                                        309 R.YS., T.M.RBAKD.BAS.MNR., SDMC.T.W.SBB.CYHMB., HN.S.RMN., BMH 250
                                                                                                                                                                                                                                                                                                                                 728 CAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTG 787
                                                                              548 GACCIGAACACCAGAIGGAAGCIICIGCAGGIGGCCGICGAGGACCGAGICAGGAGCIG 607
                                                                                                         129 MA.ABW...SCNWW..K.SHMNBC.H.SMNAA.HWKRNC.K.DB.GDYCAK.ARRN.RS. 70
                                        Gaps
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  DB 9; Length 440;
Query Match 3.2%; Score 41.8; DB 9; Length 44 Best Local Similarity 8.7%; Pred. No. 0.0013; Matches 33; Conservative 132; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908 AAGCAAAATGACCAGCCCA 926
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Local Similarity 8.7%;
les 33; Conservative 1
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Gurney, Austin L.
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Smith, Victoria
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169 TCCTGAGGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAA 228
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                                                                                                                                                                                                                                                                                                                               h 2.8%; Score 37.6; DB 9; Length 417; Similarity 53.1%; Pred. No. 0.035; 04; Conservative 0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.8%; Score 37.2; DB 9; Length 891;
48.9%; Pred. No. 0.078;
tive 0; Mismatches 133; Indels
                       FROM VARIOUS CDNA LIBRARIES
                TITLE OF INVENTION: FROM VARIOUS CDNA LIBRA CURRENT APPLICATION NUMBER: US/09/918,995 CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: US/09/235,076 NUMBER OF FLING DATE: 1999-01-20 NUMBER OF SEQ ID NOS: 38054 SEQ ID NO 3955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
FRIOR APPLICATION NUMBER: US/09/37484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENT NOS: 7059
SOFTWARE: PATENT NOS: 7059
LENGTH: 891
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Publication No. US20020197605A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIZOGUCHI, HIROSHI
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APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
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US-09-918-995-3955
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US-09-738-626-2757
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Best Local 8
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369 T...CYKHK..NHRCDWCY.WC.YYCASNKW...K.YN.A..WC.HTB.A..SB.MCMMR 310
                                                                                                     309 R.YS..T.M.RBAKD.BAS.MNR..SDMC.T.W.SBB.CYHMB...HN.S.RMN...BMH 250
                                                             668 GGTCCCTGGGAGAGAGCCATCTCGCCAAACAAGTGCCCTACTATATCAACCACGAGACT 727
                                                                                                                                                728 CAAACAACTIGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTG 787
                                                                                                                                                                              249 KW..HAKCDHS...BN.YH..CY...WMAKRM.BAHBTM.THNY..ST.CRDDC.BH.Y. 190
                                                                                                                                                                                                                                          788 AATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCC 847
                                                                                                                                                                                                                                                                      848 CITICCITGGAICTCITGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCACAACCTC 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTEEQ for Windows Version 3.0
LENGTH: 497
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
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Publication No. US20030073623A1
GENERAL INFORMATION:
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Publication No. US20030073623A1
GENERAL INFORMATION:
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: OTHER INFORMATION: n = A,T,C or G
JS-09-918-995-30349
                                                                                                                                                                                                                                                                                                                                                                                                                         908 AAGCAAAATGACCAGCCCA 926
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1234 GTTGGGTGAAGTTGCATCCTTTGGGGCAGTAACATTGAGCCAAGTGTCCGGAGCTGCTT 1293
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                                                        1174 ATTTTGTGACCAGCCAGGCTGGGCCTCCTTCTGCATGATTCTATCCAAATTCCAAGACA 1233
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                1294 CCAATTTGCTAATAATAAGCCAGAGA 1319
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Publication No. US20020197605A1
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APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
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LENGTH: 960
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489 KNWM.MS.SBBM.BAC.HAC..KBHR.CH.T.BDHBB..A.YRHBN.YM.A.CCTB.RBS 430
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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2.8%; Score 36.8; DB 9; Length 77
Best Local Similarity 9.7%; Pred. No. 0.098;
Matches 47; Conservative 144; Mismatches 294; Indels
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CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
1294 CCAATTTGCTAATAATAAGCCAGAGA 1319
                                                                                                                                             Sequence 348, Application US/10184644 publication No. US20030044930Al GENERAL INFORMATION:
                                       87 GACGTGGCCTAAAAGGAAGCCCGCGA 62
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Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
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Smith, Victoria
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ORGANISM: Homo Sapien
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US-10-184-634-348/c

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Sequence 10, Application US/10123155 Publication No. US20030068794A1
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                      APPLICANT: Warren, Wesley C.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Watanabe, Colin K
Wood, William
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Best Local Similarity 52.6%
Matches 103; Conservative
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Godowski, Paul J.
Gurney, Austin L.
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Gao, Wei-Qiang
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Smith, Victoria
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GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343041C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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  Sequence 348, Application US/10184634
Publication No. US20030068684A1
                                                                                                                                                                                                                                          Watanabe, Colin K.
                                                                                                                                  Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
                                                                   APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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ORGANISM: Homo Sapien

TYPE: PRT

US-10-184-634-348

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APPLICANT: Tao, Nengbing APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C. APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Magappan TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REPRENCE: 16511.006/37-21(10298)C CURRENT APPLICATION UNMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112
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52.6%; Pred. No. 0.12;
tive 0; Mismatches 90; Indels
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CTHER INFORMATION: Clone ID: 12-BOVMS1-020-Q1-E1-C7
US-09-960-352-2880
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                            Sequence 2580, Application US/09960352
Patent No. US20020137139A1
US-09-960-352-2580
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US-10-184-634-466
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US-10-184-634-466
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                                                                                                                                                                                     530 AACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAG 589
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                                                                           2.7%; Score 35.4; DB 9; Length 594;
                                                                                                   Best Local Similarity 8.3%; Pred. No. 0.25;
Matches 34; Conservative 147; Mismatches 230; Indels
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CURRENT FILING DATE: 2002-06-28

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                 Pred. No. 0.25;
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5. US20030044930A1
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Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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US-10-184-644-466
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-10
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61 AACTAAAGAACCIGTAATCAIGAGTACTCTIGAGACTGTACGAATATTTCTGACAGAGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 TGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCAC 540
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                                                                                                                                                 123 FPDSWVVLCTCSGMSGLITLSRNASYYLRPWPPRGSKDFSTHEIFRMEQLLTWKGTCGHR 182
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121 GCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAG 180
                                                  63 PDMGLVALEAEGQELLLELEKNHRLLAPGYIETHYGPDGOPVVLAPNHTDHCHYQGRVRG 122
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Matches 76; Conservative 129; Mismatches 349; Indels
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CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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13.7%; Pred. No. 0.31;
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Goddard, Audrey
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ORGANISM: Homo Sapien
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                                               121 GCCTTTGGAAGGACTAGGAAACTCTACCAGGAGCCCAGAGAGGTGCCTCCTGAGGAGAG 180
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                                                                                                    63 PDMGLVALEAEGQELLLELEKNHRLLAPGYIETHYGPDGQPVVLAPNHTDHCHYQGRVRG 122
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3 WRPRRARGTPLLLLLLLLLLLWPVPGAGVLQGHIPGQPVTPHWVLDGQPWRTVSLEEPVSK 62
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Patent No. US2020132237A1
GENERAL INFORMATION:
APPLICANT: AJalate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
APPLICANT: HARLOCKER, SUSTAIN COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SEQ TYARE: FastSEQ for Windows Version 4.0
LENGTH: 373
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54.8%; Pred. No. 0.41;
Live 0; Mismatches 56;
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Best Local Similarity 54.8
Matches 68; Conservative
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LOCATION: (1)...(373)
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JS-09-867-701-724
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1182 ACCAGGGGAGGCTGGGCCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTG 1241

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Search completed: April 25, 2003, 23:58:21
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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,	E30219	Shortened dystrophin.	E30219 E30219 1 GT:13017026	JP 1999318467-A/2	unidentified.	unidentified	unclassified.	1 (bases 1 to 4402)	Sinichi, T.	Shortened dystrophin	Patent: JP 1999318467-A 2 24-NOV-1999.	SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY	
RESULT 1 E30219	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	JOURNAL		

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COMMENT	Ę.	OS PN	Unidentified JP 1999318467-A/2	·A/2	- -	781 GAAAGATGATGA
		PD PF	24-NOV-1999 08-MAY-1998 JP	JP 1998142134	g do	
		F P C	SINICHI TAKEDA C12N15/09, A61K48/00, C12N1	48/00,C12N15/00	QY	841 GCAGAACGATGT
		288	Strandedness: Both; Topology: Linear;	Both;	QQ	1805
		FH	Key source	Location/Qualifiers 14402	QY	901 GAGTACTCTTGA
FEATURE	RES	FT	Location/0	/organism='Unidentified'. Qualifiers	qa	1805
	urc	O)	14402 /organism=	14402 /organism="unidentified"	ζō	961 ACTCTACCAGGA
BASE COUNT	COUNT	H	/db_xref=" 1329 a 1000 c	"taxon:32644" 1019 g 1054 t	qu	1805
ORIGIN	z				QY	1021 TCTACGAAAGCA
One	Query Match Best Local S	- 5	y Match 61.6%; Local Similarity 81.0%;	Score 1257; DB 6; Length 4402; Pred. No. 2.9e-307;	qu	1805
Mat	ches	1654;	Conservative	e d	QY	1081 TGACTGGCAGAG
		TCCTTC	ACAGCATTTGGAAGC	TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGAAGATTCATTC	qa	1848 rgacrggcagac
o vo	61	TGAAGT	AAACCTGGACCGTTA	ATCAAACAGCTTTAGAAGAAGTATTATGGTGGGTTGTTTC 120	oy D	1141 GGATGAGCTGG4
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op G	1695		TCTAGAACAAGAAC	AGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTCACTCA	qa	2388 CTCAGCTTATA 1681 CTTGAGCCTG1
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_	1805	AGGAGGTCAATACTGAGTGGGAAAATTGAACCTGCACTCCGC	84
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. ~ ^	41	GATGAGCTGGACCTCAAGCTGCGCCAA 	1200 1967
٠,	201	GGCGATCTCCTCATTGACTC	26
c	89	TCTCCAAGATCACCTCGAGAAGTCAAGGCACTTCGAG	2027
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                                        301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                 361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
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Multiple dystrophin isoforms are associated with the postsynaptic
membrane of Torpedo electric organ
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2088 CACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAG 2147
                                  1381 ATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAG 1440
                                                                                                                      GGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATT
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Dystrophin is a component of the subsynaptic membrane
J. Cell Biol. 115 (4), 1069-1076 (1991)
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on Sep 8, 1993 this sequence version replaced gi:213232.
Draft entry and computer-readable sequence for [Unpublished (1990)]
Kindly submitted
by S.J.Burden, 06-AUG-1990.
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Physiol. (Paris) 85 (3), 131-133 (1991)
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1199 GTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGA 1258
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PAT 18-JUN-2001

linear

DNA

4075 bp

E30221

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EFINITION

Shortened dystrophin. E30221 E30221.1 GI:13017028 JP 1999318467-A/4. unidentified.

> ERSION EYWORDS OURCE

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L Patent: JP 1999318467-A 4 24-NOV-1999;
SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY OS Unidentified
NN JP 1999318467-A/4
PD 24-NOV-1999
PP 08-MAY-1999 JP 1998142134
PR SINICHI TAKEDA
PC C12J15/O9-A61K48/00.C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source //organism='Unidentified'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1601 GACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAG 1660
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'organism='Unidentified'
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6e-159;
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Pred. No. 6e-

    .4075
/organism="unidentified"

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910 c 936 q
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Best Local Similarity 99.1%;
Matches 675; Conservative
                                        Sinichi,T.
Shortened dystrophin
                             (bases 1 to 4075)
unidentified
              unclassified
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ORGANISM
                                       AUTHORS
TITLE
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731 c 720 a
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Best Local Similarity 98.6
Matches 619; Conservative
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AUTHORS
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                                                                                    PAT 18-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTCTGCGTGGATA 1841
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                                                                                                                                                                                                                                                                                                                                                                                     organism='Unidentified'
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Strandedness: Both;
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                                                                                 3747 bp
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853 c 859 g
                                                                                                                                                                                                                                                                                     08-MAY-1998 JP 1998142134
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           2461 CTTCTGCATGATTCTATCCAA 2481
2021 CTTCTGCATGATTCTATCCAA 2041
                                                                                                                                                                                                                                                             JP 1999318467-A/1
                                                                                                                                                                                                                                                                                                                                                  Topology: Linear;
                                                                                                                        E30218.1 GI:13017025
JP 1999318467-A/1.
                                                                                                Shortened dystrophin. E30218
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Matches 672; Conservative
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KEYWORDS
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Datent: JP 1999318467-A 6 24-NOV-1999;
SCIENCE & TECH AGENCY,NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
OS Unidentified
PD 24-NOV-1999
PF 08-MAY-1998 JP 1998142134
PR SINICHI TAKEDA
PC CIZU15/O0,A61K48/O0,C12N15/O0
CC Strandedness: Both;
CC Topology: Linear;
FH Key
FT source
//organism='Unidentified'.
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1895 TITATGACCGCCTGGAGCAAGAGCACAACAATTGGTCAACGTCCCTCTGTGCGTGGATA 1954
                                                                                                                      1955 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCC 2014
                                                                                                                                                                      1902 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGAT 1961
                                                                                                                                                                                                                                                                   1962 ACCITITCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCGGGGCCTGGGCCTCC 2021
                                                                                                                                                                                                                                                                                               2075 ACCTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCAGGCTGGGCCTCC 2134
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                                                                                                                                                                                               2015 TGTCTTTTAAAACTGGCATCATTCCCTGTGTAAAGCACATTTGGAAGACAGTACAGT
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    .3163
/organism="unidentified"
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Dystrophin and Dp71, two products of the DMD gene, show a different pattern of expression during embryonic development in zebrafish Mech. Dev. 102 (1-2), 239-241 (2001)
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1 (bases 1 to 3521)

Bolanos-Jimenez, F., Bordais, A., Behra, M., Strahle, U., Sahel, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-JAN-2001) Laboratoire de Physiopathologie Retinienne,
EMI 99-18 INSERM-Universite Louis Pasteur, 1, Place de 1'Hopital,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="Aak38376.1"
/db_xref="G1:13699250"
/translation="RFCRHWEDSHAKLTARVLTLQNMYKDSSDWLEARKRVEPLIKKA
ACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGA 1713
                        1182 ACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGA 1241
                                                                                     CCAGCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTT 1773
                                                                                                                                                                   GACCACTATTTATGACCGCCTGGAGCAAGAACAACAATTTGGTCAACGTCCCTCTCTG 1833
                                                                                                                                                                                                             GACCACTATTTATGACCGCCTGGAGCAAAGACAAAAAATTTGGTCAACGTCCTCTCTG 1361
                                                                                                                                                                                                                                                      CGTGGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGAT 1893
                                                                                                         1894 CCGIGICCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAA 1953
                                                                                                                                                                                                                                                                                                                                                               1954 GTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCT 2013
                                                                                                                                                                                                                                                                                                                                                                                                                                               AF339031 3521 bp mRNA linear VRT 20-AP1
Danio rerio dystrophin (dmd) mRNA, partial cds, alternatively
spliced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 3521)
Bolanos-Jimenez, F., Rendon, A. and Strahle, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="between z5508 and z5058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="alternatively spliced"
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/db_xref="taxon:7955"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2014 GGGCCTCCTTCTGCATGATTCTATCCAA 2041
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Location/Qualifiers
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SOURCE

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WYKQWTESHNIAWANI KRKGONE ADLEAGLEQUAY YLDLEK FLWHLTEAETTANVL
QDATFKEGLLENPATVRHLLEQWQDLQAEIDAHRETY HSLDENGHR I VSSLEGTONA V
LOKRLDDWGQRWHEBLCKNYWSI RPYLDAGOVOWHLHENBAGDELLWHQLKREELEKQ
VLOKRLDDWGQRWHEBLCKNYWSI RPYLDAGOVOWHLHENSLOELNWLGLKREELEKQ
KPGGBVPTVHQOLLTHRARELGAKEPVI NGTLDNAKTFLAEMPRGLKQRPGGKD
VSPEERVONVGRILKKEVEDVTVRWKNIGAASVDWGQOLELALERLMELQDAGDQLDY
KLRQAESVNSWKRPVOYGELLVDDLQNHTDRYKRPOEELAPIGNUNHVNOLASTFRSD
IQLSPDALSRIDDLNMRWHLLQISIEBHLSQLTTAFRDLGPSONFLHASVESPLERSI
SPNNVPYY I NHQTQTTCWDHPKMAELYQSLADLNNVRFSAYRTAMKLRRWGKALCLDL
LSWPRAAGEREGHRIKLQUSSTEEHLSQLTTAFRDLGOGHSSLVNVPLCVDMCLNM
LLNVPYY I NHQTQTTCWDHPKMAELYQSLADLNNVRFSAYRTAMKLRRWGKALCLDL
LSWPRAAGEREGHRIKLQUSSTEENSTOONSTELSCOORSIGALLH
DAIQIPROLGEVASFGGSNLEEDSVRSCFOFANNKPELEASVFLDWMRLEDCLLH
LHVPAAABTAKHQAKCNICKECPIIGFRY RSLKHFNYDICQSCFFSGRVAKGHKMQYP
WYRYCTPTTSGEDVRDFAKVLKNFFRYRFRYFFRYPRYDTICQSCFFSGRVAKGHKMQYP
WYRYCTPTTSGEDVRDFAKVLKNFFRYRFRYFFRYPRYDTICGSCFFSGRVAKGHKMQYP
WYRYCTPTTSGEDVRDFAKVLKNFFRYRFRYFFRYPRYDTICGSCFFSGRVAKGHKMQYP
WYRYCTPTTSGEDVRDFAKVLKNFFRYRFRYFFRYPRYDTICGSCFFSGRVAKGHKMQYP
WYRYCTPTTSGEDVRDFAKVLKNFFRYRFRYFFRYPRYDTICGSCFFSGRVAGHKMQYP
WYRYCTPTTSGEDVRDFAKVLKNFFRYRFRYFRYPRYDTICGSCFFSGRVAGHKMQYP
WYRYCTPTTSGEDVRDFAKVLKNFFRYRFTYFRYPRYDTICGSCFFSGRVAGHKMQYP
WYRYCTPTTSGEDVRDFAKVLKNFFRYRFTYFTYFTTOWYNCGFFSGROAGHKNOYP
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ILISWETEEKGELERVLNDLEQENRKLQAEYDRLKKAHDHKGLSPLOSPPQMLPVSPQ
SPRDAELIAEAKLLRQHKGRLEARMQILEDHNKQLESQLTRLRQLLEGTESKVNGTAL
NEKLESWKKVSHSVEDLKGQNADVKQL,SKDLQQWQTQMNVTNELANKLLTLYADDDTS
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linear ROD 27-APR-1993
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3275)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1874 ACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGT 1933
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                                                                                                                                                                                     1454 GCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCA 1513
                                                                                                                                                                                                                                                      1514 AACAAAGTGCCCTACTATATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAA 1573
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                                                 1334 CAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTG 1393
                                                                    1394 CAGGIGGCCGICGAGGACCGAGICAGGCAGCIGCAIGAAGCCCACAGGGACITIGGICCA 1453
                                                                                                                                          1472 cccrcrcasaarrrccrrcarscsrcrsrrsaascccrcrcsaacscrcrarrrcacc 1531
mRNA
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88018015
3659917
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Mouse adult heart, cDNA to mRNA.
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AGLDKTVSLQKDLSEWHEWMTQAEEEYLERDFEYKTPDELQTAVEEMKRAKEEALQKE
TKVKLLTETVNSVIAHAPPSAQEALKKELETLTTNYQWLCTRLNGKCKTLEEVWACWH
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                                                                                                                                                             LOLGSOLVGKGKLSEDEEAEVQEQMNLLNSRWECLRYASMERQSKLHKVLMDLQNQKL
KELHDWLTKTEERTTKRMEEEPFGPDLEDLKCQVQQHKVLQEDLEQEQGVRVNSLTHMVV
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WLSEKEDAWKNIQTSGFKDQNEMMSSLHKISTLKIDLEKKKPTWEKLSSLNQDLLSAL
                                                                                                                                                                                                                                                                                              AVYRKEGIISELOGEKWAIAREKAEKFRKLODASRSAQALVEOMANEGVNAEGIRQAS
BOLNSRATERCOLLSERVNWLEYQTWAITFYROLLGOGEMENTTABENLLKTGSTTLSEP
TALKSQLKICKDEVNRISALOGOIEOUKIOSLOLKEKGOGPMELDADEVAFTHRENLI
FDGVRAKEKELOZIFDTLEPPMRYQETMSSIRTWIQQSESKLSYPZLSYTEYETMERKI
                                                                                                                                                                                                                                                                                                                                                                             GKLOALOSSIKEOONGFNYLSDTVKEWAKKAPSEICOKYLSEFEEIEGHWKKLSSOLV
ESCOKLEEHMNKLRKFONHIKTLOKWWAEVDVFLKEEWPALGDAEILKKOLKOCRLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELLSYLEKANKWINEVELKIKTMENVPAGPEEITEVLESLENLMHISEENPNOIRLIA
OTLTDGGVMDELINEELETFNSRWRELHEEAVRKOKLLEOSIQSAQEIEKSLHLIQES
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TREQIMVKHAGEELPPPPPOKKRQITVDSELRKRLDVDITELHSWITRSEAVLQSSEF
                                                                                                                                                                                                                                                                                                                                                                                                                          GDIQTIQPSLNSVNEGGQKIKSEAELEFASRLETELRELNTQWDHICRQVYTRKEALK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 ACAGTTTCATGCTCATGAGGATTCATGATGATCTGACACTCTCATCAAGACTTGTTGG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 585.8; DB 10; Length 3275;
Pred. No. 2.9e-137;
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                                                               /codon_start=3
/protein_id="AAA37530.1"
/db_xref="G1:192972"
/db_xref="taxon:10090"
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                                             /note="dystrophin"
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Best Local Similarity 83.4%;
Matches 665; Conservative (
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/translation="MQILRTLQKCGKLKMMAVVRTSLQKVVVLLHRLQRMAVSSPRYQ
KLCKDIQAEIDAHNDIFKSIDGNRQKMVKALGNSEEATMLQHRLDDMNQRWNDLKAKS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3161)
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TGATGAATCTAGTGGAGATCACGCAACTGCTTTTGGAAGAACAACTTAAGGTATTGGG 660
                                                                                                                                                               661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACAG 720
                                                                               662 TGATGAATCCAGCGGTGATCATGCAACAGCTGCTTTGGAAGAACAACTTAAGGTACTGGG 721
                                                                                                                                                                                                                721 ITCTGACCAGIGGAAGCGICIGCACCIITCTCIGCAGGAACTICIGGIGIGGCTACAGCI 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blake, D.J., Schoffeld, J.N., Zuellig, R.A., Gorecki, D.C., Phelps, S.R., Barnard, E.A., Edwards, Y.H. and Davies, K.E. G-utrophin, the autosomal homologue of dystrophin Dpl16, is expressed in sensory ganglia and brain Proc. Natl. Acad. Sci. U.S.A. 92 (9), 3697-3701 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="G-utrophin (predicted protein)"
/protein_id="CAA58496.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
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/clone_lib="adult mouse brain"
/dev_stage="adult"
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/db_xref="MGD:MGI:104631"
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/db_xref="taxon:10090"
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REMARK

SOURCE

FEATURES

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PHDDTHSRIEQYATRLAQMERTNGSFLTDSSSTTGSVEDBHALIQQYCQTLGGESPYS
QPQSPAQILKSVEREERGELERIIADLEEEQRNLQVEYEQLKEQHLRRGLEVGSPPDS
IVSPHHYSEDSELIAEAKLLRQHKGRLEARMOILEDHNKQLESQLHRLRQLLEQPDSD
SRINGVSPWASPQHSALSYSLDTDPGPQFHQAASEDLLAPPHDTSTDLTDVMEQINST
                   CNICKEC PIVGFRYRSLKHFNYDVCQSCFFSGRTAKGHKLHYPMVEYCIPTTSGEDVR
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GGSNIEPSVRSCFQQNNNKPEISVKEFIDWMHLEPQSMVWLPVLHRVAAAETAKHQAK
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                          1412 ATCCCTTGCTGATCTCAATAATGTACGTTTCTCTGCCTACCGCACAGCAATCAAAATTCG 1471
1352 CATCAACCATCAAACACAGACAAGCTGTTGGGATCATCCTAAAATGACTGAGCTCTTCCA 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus dystrophin-related protein 2 B-form splice variant (Drp2) mRNA, complete cds.
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Mol. Cell. Neurosci. 16 (5), 674-685 (2000)
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Roberts, R.G. and Sheng, M.
Direct Submission
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Roberts, R.G. and Sheng, M.
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TSGKLQLPLOEI IDWLSQKDEELSAQLPLGGDVALVQDEKETHAARPHEBVESKGPYIY
RSGKLQLPLOEI IDWLSQKDEELSAQLPLGGDVALVQDEKETHAARPHEBVESKGPYIY
SVLESAQAELSQHPEELEESHSESKROTSPRORIONLSRFWWQATVASELWEKLTAR
CVDQHRHITEHTLEILOGAMEELSSTUTYQAEGVRATWEPIGDLFUDLPEHIQAIK
CVDQHRHITEHTLEILLIGOGAMEELSSTUTYQAEGVRATWEPIGDLFUDLPHIQAIK
LGDARRDFGGEGSQHLSTSVQVPWERAISPNKYPY THAQAGTTCWDHPKWTELYQTL
ADLNNIKFSAYRTAMKLRRVQKALLDLDVTLTTALEIFNEHDLQASEHYMDVVEVIHC
ADLNNIKFSAYRTAMKLRRVQKALLDLDVTLTTALEIFNEHDLQASEHYMDVVEVIHC
LTALYERLEBERSTUNVNSGSKCDQRHLGALLHEATJOVPROLGEVAAFGSNVEPSVRGFRF
KRKLQYLFSQVARSSKCORHLGALLHEATJOVPROLGEVAAFGSNVEPSVRGFRF
STGKPVRDICQTCFLTGRASKONKLHYPIMEYYTPTTSSENMRDFATTLKNKFRSKQY
SLKQPRVDICQTCFLTGRASKONKLHYPIMEYYTPTTSSENMRDFATTLKNKFRSKQY
FEKHOORGYLENGSSKCONGTPRICT
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LQGELRRLKWQHBEAVEAPTLAEGSREATPDHRNEELLAEARILROHKSRLETRWQIL
EDHNKQLESQLQRLRELLLQPPTESDGNGSAGSSLASSPRQSEGSHPREKGQTTPDTE
AADDVGSKSQDVSHSLEDIMEKLRHAFPSVRSSDVTANTLLAS"
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/note="DRP2; membrane-associated cytoskeletal protein; contains two spectrin repeats; WW domain; 22 domain" /codon_start=1
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
1074 IGAAIGACCIGGCCCACCAGCTIGCTATITCTGAIGIGCACTIGICAAIGGAGAAITCAA 1133
                          1356 GCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAG 1415
                                         1536 ACCACGAGACTCAAACATGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTT 1595
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                                                                                                                                                                                                                                                                                                                                                                      1494 AGCACGACTIGCAGGCCAGIGAACAIGIAAIGGAIGIGGIGGAGGICAIICACIGCIIGA 1553
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Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds.
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Association of dystrophin-related protein 2 (DRP2) with postsynaptic densities in rat brain Mol. Cell. Neurosci. 16 (5), 674-685 (2000)
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Roberts, R.G. and Sheng, M.
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CVDQHRHIEHTLEILGEIGGAMEELSSTLTQARGVRATWEBIGDLEIDSLEBHIGAIR
CVDQHRHIEHTLEILLEIGGAMEELSSTLTQARGVRATWEBIGDLEIDSLEBHIGAIR
LEKEEFSPKDGWLLVNDLAHGLAISVHLASKBNSRALEQINVRWKQLQVSVAERLKQ
LQDAHRDFGPGSQHFLSTSVQVPWERAISPNKVPYINHOAGVTCWDHPKWFRELYQTL
ADLNNIKFSAYRTAMKLRRVOKALRLDLVTLTTALEIRNEHDLQASEHVMDVVEVIHC
LTALYRELEEERGILVNVPLCVDMSLANGLHASTORPHOAGTGCRAFGGSNVESVRSCFRF
SKRQFVLESQVANGSKCDQRHLGALLHASIQVPRQLGEVAAFGGSNVESVRSCFRF
STGKPVTEASOFLEWVNLEPGSMWLAVPLRYVTASEQVKHQTKCSICRQCPIKGFRYR
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FSKHPQRGYLPVQSYLESCOSSWPALANGSPRADTHSRIEHFASRLAEMSGONCSFFN
LQGELRRLKWQHEEAVARAFLAGGSARATDHRNBEELAARILRQHKSRLETRMOIL
EDHNKQLESQLORLELLQPPTESDGNGSAGSSLASSPRQSEGSHPREKGQTTPDTFE
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TIPAPPWDGAGDPCLSPKLLNGSVGAVGPLEPSAMNLCWNEIKKKSHNLRAELEAFSD
HSGKLQLPLQEIIDWLSQKDEELSAQLPLQGDVALVQQEKETHAAFMEEVKSKGPYIY
Direct Submission Submitted (18-OCT-1999) Division of Medical and Molecular Genetics, GRT Medical School, 8th Floor, Guy's Hospital, Guy's Tower, London SEI 9FT, UK
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                                                                                                                                                                                                                                                                                                 /gene="Drp2"
267. 3140
/gene="Drp2"
/note="DRP2; membrane-associated cytoskeletal protein;
contains two spectrin repeats; WW domain; ZZ domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="dystrophin-related protein 2 A-form splice
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/db_xref="G1:11066165"
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/db_xref="taxon:10116"
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HSU43519 3499 bp mRNA linear PRI 15-JUN-1996 Human dystrophin-related protein 2 (DRP2) mRNA, complete cds.
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SPDDSIDEDQYLLRHSSPITDREPAFGQQAPCSVATESKGELQKILAHLEDENRILQG
ELRRIKWQHEEAAAEAPSLADGSTEAATDHRNEELLABARILKQHKSRLETRWQILEDH
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 263 to 3189)
                                                                                                                        Roberts, K.G., Freeman, T.C., Kendall, E., Vetrie, D.L., Dixon, A.K., Shaw-Smith, C., Bone, Q. and Bobrow, M. Characterization of DRP2, a novel human dystrophin homologue Nat. Genet. 13 (2), 223-226 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                 Roberts.R.G.
Direct Submission
Submitted (16-DEC-1995) Roland G. Roberts, Medical Genetics, Submitted (16-DEC-1995) Roland G. Roberts, Addenbrooke's Hospital, 3rd Floor, Lab Block, Addenbrooke's Hospital, Hills Road, Cambridge, Cambs Cb2 20q, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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/protein_id="AAC50538.1"
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                                                        996 AGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGT 1055
                                                                                                                                        GGGAGAAGTTGACAGCCCGCTGTGTGGACCAGCACCGTCACATTGAGCGGACTCTGGAGC 1012
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                                                                                                                                                                                                                      1176 TGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACC 1235
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                            833 AGCACCCATTTGAGGAGTTAGAGGAGCCTCATTCTGAGAGCAAAGATACCTCCCCGAAAC 892
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2110)

Lederfein, D., Levy, Z., Augier, N., Mornet, D., Morris, G., Fuchs, O., Yaffe, D. and Nudel, U.

A 71-kilodalton protein is a major product of the Duchenne muscular dystrophy gene in brain and other nonmuscle tissues

Proc. Natl. Acad. Sci. U.S.A. 89 (12), 5346-5350 (1992)
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LEPOSMWALD-VLHRVAAAFTAKHOAKCNI CKRCPI I GERYRSLKHFNYDI COSCFFSG

RVAKGHKMHY PMVSTCTPTTSGEDVRDAKVILKKRTKRYFKFAKHPRWICTLEVOTVLE

CONMETPASSPOLSHDTSS LEHYARLAEBENSNGSYLNDSI SPINESI DDFHLLI O

HYCOSLNODSPELSOPRSPAQIL I SLESEERGELERI LADLEEENRILOAFYDRLKQOH

HRKGLISPLPSPPEMMPTSPOSPRAAELI AFAKLILARDKINGLERAROI LEBDINKOLESO

LHRLCLEOVOROPSYNOTTYSSPSTSLORSOSSOPMILLRVVGSOTSDSMGEEDLIS

PPODTSTGLEEVMEOLINISPSSRGHNVGSLFHMADDLGRAMSILVSVWTDEEGAE
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RRLQKALCLDLLSLSAACDALDQHNLKQNDQPMDILQIINCLTTIYDRLEQEHNNLVN
VPLCVDMCLNWLLNVYDTGRTGRIRVLSFKTGIISLCKAHLEDKYRYLFKQVASSTGF
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                                                                                                                                                                 HUMDMDXX 2110 bp mRNA linear PRI 07-19 Human Duchenne muscular dystrophy (DMD) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                   Duchenne muscular dystrophy protein.
Homo sapiens brain cDNA to mRNA.
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/db_xref="taxon:9606"
/map="Xp21.3-p21.1"
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/db_xref="G1:181599"
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1. .2110
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/gene="DMD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC028720 4658 bp mRNA linear PRI 01-MAY-2000 types), clone MGC:33083 IMAGE:4822807, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4658)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                     1957 CAGATACCITITICAAGCAAGTGGCAAGTICAACAGGAITITGTGACCAGCGCAGGCTGGG 2016
                                                                                                                                 1777 CACTATTATGACCGCCTGGAGCAAGAGCACAACTTGGTCAACGTCCCTCTCTGGGT 1836
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                                                                                                                                                                                                                                                                                                              TGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1956
                                          1717 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1776
                                                               313 CACTATTTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGT 372
193 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Milos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tosha Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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/clone="MGC:33083 IMAGE:4822807"
/tissue_type="Testis"
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/db_xref="LocusID:1756"
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/lab_host="DH108"
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                                                                                 /product="dystrophin (muscular dystrophy, Duchenne and Becker types)"
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Human fetal mRNA fragment of DMD gene (DMD= Duchenne muscular
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ilarity 100.0%; Pred. No. 8.4e-117;
Conservative 0; Mismatches 0;
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note="Vector: pBluescript"
                                                                                                                                                                       /protein_id="AAH28720.1"
/db_xref="GI:20379676"
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X06179 M22819
X06179.1 GI:30839
Duchenne muscular dystrophy.
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Homo sapiens

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/translation="SKLIGTGKLSEDEETEVQEQMNLINSRWECLRVASMEKQSNLHR
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RVNSLTHMYVVVDESSGDHATAALEEQLKVLGDRWANICRWTEDRWVLLQDTLLKWQR
LTEEQCLFSAWLSEKEDAVNKIHTTGFKDQNEMLSSLQKLAVLKADLKK"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 630)

Cross, G.S., Speer, A., Rosenthal, A., Forrest, S.M., Smith, T.J., Pelavards, Y., Flint, T., Hill, D. and Davies, K.E.
Deletions of fetal and adult muscle cDNA in Duchenne and Becker EMBO J. 6 (11), 3277-3283 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 AGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAG 319
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                                                                                                                                                            Data kindly reviewed (12.0CT.1988) by DAVIES K.E.
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/clone="Cf16."
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                          New dystrophin minigene for treating Duchenne or Becker muscular
dystrophy comprises an N-terminal domain or modified N-terminal domain,
                                                                                   Human dystrophin minigene delta3510.
                   AAD37240 standard; DNA; 3510 BP.
                                                                                                                                                                                                                 27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                       28-APR-2000; 2000US-200777P.
                                                             21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                     WPI; 2002-049342/06.
                                                                                                                                                                        WO200183695-A2.
                                                                                                                                                                                                                                                              (XIAO/) XIAO X.
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                             08-NOV-2001.
                                          AAD37240;
                                                                                                                                                                                                                                                                                   Xiao X;
RESULT 1
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rod repeats, H1 and H4 domains and a cysteine rich domain of

dystrophin gene

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domarins and cysteine-rich domains and cysteine-rich comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3310 containing nucleotides 1-1668 (N-terminus, hinge HI and rods RI and R2), 8407-110227 (rods R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids). Example 1; Page 51-52; 71pp; English.

Sequence 3510 BP; 1073 A; 787 C; 828 G; 822 T; 0 other;

0; Gaps 100.0%; Score 2041; DB 24; Length 3510; 0; Indels ; Pred. No. 0; 0; Mismatches 100.08; Matches 2041; Conservative Best Local Similarity

1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60

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61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120

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1440 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 1499 481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 540 ò g

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1620 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTACAAGACAG 1679

8

1801 AGAGCACAACAATTTGGTCAACGTCCCTCTGCGTGGATATGTGTCTGAACTGGCTGCT 1860

2700 GCCCAIGGATATCCTGCAGATTATTAATTGTTTGACCACTATTATGACGCCTGGAGCA 2759

CITGAGCCIGICAGCIGCAIGIGAIGCCIIGGACCAGCACCACCACAAAGCAAAAIGACCA 1740

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2640 crigasccrercascrecarersarsccrresaccascascascasascaaarsacca 2699 GCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCA 1800

CTCAGGITATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCT 1680 GGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATT 1620 1441 GGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAG 1500 AGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACAACTTGCTG 1560 CTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCT 2639 1201 GGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGG 1260 1261 AGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTAC 1320 1321 CACTITGGGCATICAGCICICACCGIAIAACCICAGCACICIGGAAGACCIGAACACAG 1380 1021 TCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGC 1080 1081 TGACTGGCAGAAAAAAAAAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCAC 1140 2040 TGACTIGGCAGAAAAAAAAAAGATGAAGCCCTTGAAAGACTCCAGGAACTTCAAGAGGCCAC 2099 901 GAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAA 960 781 GAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGGGACTTTCCAGCAGTTCAGAA 840 721 ITCTGACCAGTGGAAGCGTCTGCACCTTTCTGCAGGAACTTCTGGTGTGGGCTACAGCT 780 2280 CACTTTGGGCATTCAGCTCTCACGTATAACCTCAGCACTCTGGAAGACCTGAACACAG GCAGAACGAIGIACAIAGGGCCTTCAAGAGGGAATIGAAAACTAAAGAACCIGTAATCAT 961 ACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGTCACTCGGCT 1680 ITCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCT 2460 1561 2520 1501 1621 Db δy Dp ò g δ g Qγ g qq δ Dp Óλ pp δλ ŏ q g ά δλ δλ qq ŏ δ QQ a Qγ

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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
Becker muscular dystrophy; ds.
2760 AGAGCACAACAATTTGGTCAACGTCCCTCTCGCGTGGATATGTGTCTGAACTGGCTGCT 2819
                       1861 GAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTTAAAACTGGCAT 1920
                                1981 AAGITCAACAGGATITTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGATTCTATCCA 2040
                                                                                               2940 AAGTTCAACAGGATTTGTGACCAGGCAGGCTGGGCCTCCTTCTGCATGATTCTATCCA 2999
                                                                                                                                                                                                                         Adeno-associated virus vector plasmid, AAV-MCK-3510.
                                                                                                                                                                          AAD37259 standard; DNA; 4476 BP.
                                                                                                                                                                                                                                                                                                                              27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                              28-APR-2000; 2000US-200777P
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                        Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-049342/06
                                                                                                                                                                                                                                                                                                WO200183695-A2.
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a Example 1; Page 63-65; 71pp; English. dystrophin gene

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control control lement, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polya signal sequence.

Sequence 4476 BP; 1252 A; 1096 C; 1127 G; 1001 T; 0 other;

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                                                             61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGAAGTATTATCGTGGCTTTTTC 120
                                                                                                                                                121 TGCTGAGGACACATTGCAAGGACACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                181 CCAGTITCATACTCATGAGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                               2136 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAAGAAGAAAAAAATGGAGGAAGA 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2196 GCCTCTTGGACCTGATCTTGAGGCCTAAAACGCCAAGTACAACAACAACATAAGGTGCTTCA 2255
                                                                                                                                                                                                                                                                                                                                                   361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAACT 420
                                                                                                                                                                                                                                                                                                                                                                                                  421 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAGA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
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                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961 ACTCTACCAGGAGCCCAGAGAGCTGCCTCAGGAGAGGCCCAGAATGTCACTCGGCT 1020
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     DB 24; Length 4476;
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                                GGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGT 1200
                                                                                          1201 GGGCGATCTCCTCATGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGG 1260
                                                                                                                                     2976 AGAAATTGCCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCCCGCCAGCTTAC 3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3336 CTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCT
2736 TCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACTGCACTCGG
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domains of second or a compression comprising dystrophin minigene operably linked to an expression control element, in a mammalian tadeno-associated virus or retrovirus is control element, in a mammalian dystrophy (DMD) and Becker muscular dystrophin minigene muscular dystrophy (DMD) and Becker muscular dystrophin minigene delta3531 containing nucleotides 1-1341 (N-terminus, dystrophin minigene delta3531 containing nucleotides 1-1341 (N-terminus, hinge H1 and rod R1), 8059-10227 (rods R22, R23 and R24, hinge H4 and cR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1020 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 50-51; 71pp; English.
                                                                                                                Human dystrophin minigene delta3531.
                                                                                                                                                                                Becker muscular dystrophy; ds.
            AAD37238 standard; DNA; 3531
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                                                                                                                                                                                                                            1560 TGAAAACAGCCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGAGTCCTGTTACA 1619
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                                                             361 TAGCATGGAAAACAAAGCAATTTACATAGAGTT-----TTAATGGATCTCCAGAATCA 414
                                                                                                  415 GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAATGGA 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1000 AGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGA 1059
                                                                                                                                                                       595 GGTAGTTGATGA-----ATCTAGTGGAGATCACGCAACTGCTGCTTGGAAGA 642
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                                                                                                                                                                                                                                                                                 700 CIGGGIICITITACAAGACAGITCIGACCAGIGGAAGCGICTGCACCIITCICIGCAGGA 759
                                                                                                                                                                                                                                                                                                                     820 CGACTTICCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAA 879
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2280 IGACCTIGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGGAC 2339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                 1720 CAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCAC 1779
                                                                                                                                                                                                                                                                                                                                                                                                                         1780 TATTTATGACCGCCTGGÁGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGA 1839
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                                                                                                           Adeno-associated virus vector plasmid, AAV-MCK-3531,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2020 CCTTCTGCATGATTCTATCCAA 2041
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28-APR-2000; 2000US-200777P.
              WPI; 2002-049342/06
      (XIAO/) XIAO X.
          Kiao X;
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin gene. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV dystrophy (BMD) in a mammalian subject. The present sequence is AAV ector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence. New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a Example 1; Page 62-63; 71pp; English. dystrophin gene

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Sequence 4498 BP; 1251 A; 1118 C; 1123 G; 1006 T; 0 other;

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2197 GGATGCTACCCGTAAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAA 2256 2077 TAGCATGGAAAAACAAAGCAATTTACATAGAACTCATAGATTACTGCAACAGTTCCCCCT 2136 GGACCTGGAAAAGTTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACA 2196 1717 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 1776 1777 IGAAGTAAACCIGGACCGTIATCAAACAGCITIAGAAGAAGIAITAICGIGGCITCTIIC 1836 475 GGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACAACAAGGT 534 TAGCATGGAAAAACAAAGCAATTTACATAGAGTT-----TTAATGGATCTCCAGAATCA 414 240 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300 61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120 121 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180 1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG Query Match 82.8%; Score 1690.8; DB 24; Length 4498; Best Local Similarity 89.9%; Pred. No. 0; Matches 1854; Conservative 0; Mismatches 187; ThADIS 11. <u>_</u> = = = = 1897 241 1957 301 361 2137 181 g q δ δy ò Ω ö g q ò g δ ò

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1540 CGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGC 1599
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                                                                                                                                          2377 AAGACGTITGGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACAT 2436
                                                                                                                                                                                                2317 TGAAAACAGCCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACA 2376
2257 ACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGA 2316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    940 GCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAG 999
                                                                                                                                                                                                                                                 760 ACTICIGGIGIGGCIACAGCIGAAAGAIGAIGAATIAAGCCGGCAGGCACCTAITGGAGG 819
                                                                                                                                                                                                                                                                                                                         820 CGACTTICCAGCAGIICAGAAGCAGAACGAIGTACATAGGGCCTTCAAGAGGGAATIGAA 879
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                                    595 GGTAGTTGATGA------ATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGA
                                                                                                          643 ACAACITAAAGG----TATIGGGAGAICGAIGGGCAAACAICIGIAGAIGGACAGAAGACCG
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1660 GAAGGCCCTITGCTIGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCA 1719
            CAACCICAAGCAAAAIGACCAGCCCAIGGAIAICCIGCAGAIIAIIAAIIGIIIGACCAC 1779
                                                             TATTTATGACCGCCTGGAGCAAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGA 1839
                                                                                                        TATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGT 1899
                                                                                                                                                       1900 CCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAG 1959
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Homo sapiens.
WO200183695-A2.
08-NOV-2001.
27-APR-2001; 2001WO-US13677.
28-APR-2000; 2000US-200777P.
(XIAO/) XIAO X.

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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -

WPI; 2002-049342/06.

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XFFFFX

Example 1; Page 48-49; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains. Tod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control

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element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta3849 containing nuclectides 1-1668 (N-terminus, hinge H1 and rods R1, R2), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                        1020 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGAATATTATCGTGGCTTCTTTC 1079
                                                                                                                                                                                                                                                                                                                                                               61 IGAAGTAAACCIGGACCGITAATCAAACAGCITTAGAAGAAGTATTATCGTGGCTTCTTC 120
                                                                                                                                                                                                                                                                                                                                             121 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGCTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                          181 CCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                           85.4%; Pred. No. U;
tive 0; Mismatches 0; Indels 348; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1740 AGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGGTAAGGAAAGGCTCCTAGAAGA 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1800 CTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGC 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGA--- 717
                                                                                                                                                              82.5%; Score 1683; DB 24; Length 3858;
85.4%; Pred. No. 0;
                                                                                                                           Sequence 3858 BP; 1189 A; 866 C; 905 G; 898 T; 0 other;
                                                                                                                                                                      Best Local Similarity 85.4
Matches 2041; Conservative
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ء .	ع ا	PCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCTGGA 1919	
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۵	1920 A	AGGITCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAG 1979	
>-	718 -	732 HILLIIIII	
q	1980 T	20	
<u>م</u> م	733 G	GAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAGATGATGA 792 	
5 Q	793 8	ATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGT 852 	
ξ, q	853 160	ACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGA 912 	
<u></u> ≵ 90	13	GACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAACTCTACCAGGA 972 	
7.7 Op	973	GCCCAGAGAGCTGCCTCCTGAGGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCA 1032 	
2 8	033	GCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCGGCTGACTGGCAGAG 109; 	21 5
i i i	093	ACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 115	2 6
λŏ	153	CCCAACCTGAGGTGATCAAGGGATCCTGGCAGCCGGTGGGCGATCTCCT 121.	2 6
δ d	213	CATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCC 127 	6 5
y d	273	TCTGAAAGAGAACGTGAGCCAC	2 5
ري م ج	33	H-F	8 8
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े ठ ट	45	AGCATCTCAGCACTTTCTTTCCAC	0 0
8 6	51	AAACAAAGTGCCTACTATATCAACCA 	থ ক
Qy Db	57 88	AATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAG 16.	32 39

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                 1753 CCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCAAACAA 1812
                                                                                                                        1813 ITTGGTCAACGTCCCTCTGCGTGGATAIGTGTCTGAACTGGCTGCTGAATGTTATGA 1872
1633 GACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTC 1692
               3300 AITITGTGACCAGCGCAGGCTGGCCTCCTTCTGCATGATTCTATCCAA 3348
                                                                                                                                                                                                                                                                                                                             1993 ATTTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGATTCTATCCAA 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adeno-associated virus vector plasmid, AAV-MCK-delta3849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 61-62; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAD37257 standard; DNA; 4825 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (XIAO/) XIAO X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD37257;
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element. The dystrophin minigene in operable linka control element, in a recombinant adeno-associated useful for treating Duchenne muscular dystrophy (D dystrophy (BMD) in a mammalian subject. The presenvector plasmid construct containing human dystrophy creatine kinase (MCK) promoter and a small polyA s Query Match Best Local Similar Matches 2041; Cor 121 TGCTGAGGA 241 TAATATTCT 541 AGAAGATCTA 2497 AGCTGAAACA 1777 TGAAGTAAA 2257 AGAAGATCTA 601 TGATGAATCT 2437 TCATAGATTA 2557 CTCCAAGGGA Sequence 4825 1 TCCTTCAC 1717 TCCTTCACE 61 TGAAGTAA 1837 TGCTGAGGA 1897 CCAGTTTCA 301 AACTGAAGT 2017 AACTGAAGT 361 TAGCATGGA 2077 TAGCATGGA 481 GCCTCTTGG 2197 GCCTCTTGG 2317 TGATGAATCT 181 CCAGITICA 718 -----718 -----718 -----Db 8888888888 ò δ qq δ рp QQ οy Qγ QΩ Óγ Ωp δλ qq ð ð ð

a recombinant adeno-associated virus or retrovirus	Qy	718
ating Duchenne muscular dystrophy (DMD) and Be) in a mammalian subject. The present sequence	Dβ	2617 TCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATGAAAAAAAA
ning human dystrophin minigenes, and a small polyA signal sequence	OY	717
BP; 1369 A; 1175 C; 1204 G; 1077 T; 0 other;	qa	2677 AGGITCCGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAG 2736
82.5%; Score 1683; DB 24; Length 4825;	δλ	73
onservative 0; Mismatches 0; Indels 348; Gaps 1;	qa	7 IGAACITCGGAAAAAGICTCTCAACATTAGGTCCCAITTGGAAGCCAGITCIGACCAGIG 2
AGCATTIGGAAGCTCCTGAAGACAAGTCATTIGGCAGTTCATIGATGAGAG 60 	Qy Db	733 GAAGCGICTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGGTACAGCTGAAAGATGATGA 792
TTTC 1 TTTC 1	QY	852
ACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAGA 180 	QY	912
NTACTCATGAGGGGTACATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240 	QY Db	972 303
ACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300 	Q _Y	973 GCCCAGAGAGCTGCCTCCTGAGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCA 1032
ACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360 	Oy Db	3
	Qy	115
GAATGACTGGCTAACAAAAAGAAGAAGAAGAAGAAGAAAATGGAGGAAGA 480 	Qy	121 327
ACCTGATCTTGAAGACCTAAAACGCCAAGTACAACATAAGGTGCTTCA 540 	Qy	1213 CATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTGGAGGAGAAATTGCGCC 1272
NGAACAAGAACAAGTCAGGGTCAATTCTCTCACTCACATGGTGGTGGTAGT 600 	Qy	133 339
PAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGG 660 	Qy	1333 TCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCT 1392
SGCAAACATCTGTAGATGGACAGAAGACCGGTGGGTTCTTTTACAAGA 717 	QY	1393 GCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCATGAAGCCCACAGGACTTTGGTCC 1452
CTGCAACAGTTCCCCCTGGACCTGGAAAGTTTCTTGCCTGGCTTACAGA 2496	Qy	
actgccaatgtcctacaggatgctaccgtaaggaaaggctcctagaaga 2556	da Db	m ~
717	Qy Dp	1573 AATGACAGAGCTCTACCAGTCTTTAGCTGACTGAATAATGTCAGATTCTCAGCTTATAG 1632
OTTERNOOT CALCARACAAGACCTCCAAGGTGAAATTGAAGC 2616	Qy	633

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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                           1753 CCTGCAGALTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAA 1812
                                                                                        TTTGGTCAACGTCCCTCTCTGCGTGCATATGTGTCTGAACTGGCTGCTGAATGTTTATGA 1872
                                                                                                                                             TITGGICAACGICCCICICIGCGIGGATATGIGICIGAACIGGCIGCIGAATGITIATGA 3936
                                                                                                                                                                    1873 TACGGGACGAACAGGGAGGATCCGTGTCCTTTTTAAAACTGGCATCATTTCCCTGTG 1932
                                                                                                                                                                                3937 TACGGGACGAACAGGAGGAGGATCCTGTCTTTTTAAACTGGCATCATTTCCCTGTG 3996
                                                                                                                                                                                                                 1693 AGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGACCAGCCCATGGATAT 1752
Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3849.
                                                                                                                                                                                                                                                            Example 1; Page 68-70; 71pp; English.
                                                                                                                                                                                                                                                                                                                                             AAD37263 standard; DNA; 4848 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric - Cytomegalovirus.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rod repeats, Hl
dystrophin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200183695-A2.
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                                                                                                                                                                                                                                                                                                                                                                     AAD37263;
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control

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element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2460 TCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACAGA 2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2520 AGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCGGTAAGGAAAGGCTCCTAGAAGA 2579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2580 CICCAAGGGAGTAAAAGAGCIGAIGAAACAAIGGCAAGACCICCAAGGIGAAAIIGAAGC 2639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2220 GCCTCTTGGACCTGATCTTGAAGACCTAAAAGCCCAAGTACAAGAACATAAAGGTGCTTCA 2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 TGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 AGATCGATGGCCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGA--- 717
                                                                                                                                                                                                             361 TAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAAACT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                                                                                                       181 CCAGTITCATACTCATGAGGGGIACAIGATGGATTIGACAGCCCATCAGGGCCGGGITGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                                                       61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
                                                                                                                                                                                             1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                          cytomegalovirus (CMV) promoter and a small polyA signal sequence.
                                                                                                                                                                     0; Indels 348;
                                                                                                                                     DB 24; Length 4848;
                                                                                                        Sequence 4848 BP; 1405 A; 1144 C; 1180 G; 1119 T; 0 other;
                                                                                                                                                                         0; Mismatches
                                                                                                                                        Query Match 82.5%; Score 1683; Best Local Similarity 85.4%; Pred. No. 0; Matches 2041; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
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9 2	2640	U TCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTGGA	2699
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QQ	2700) AGGTICCGATGATGCAGICCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAG	2759
δλ	718	TOPON	732
qq	2760	TGAACTTCGGAAAAGTCTCTCAACATTAGGTCCCATTTGGAAGCCAGT	2819
δy	73	GAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGA	792
С	7	GAAGCGTCTGCTTTCTCTGCAGGAACTTCTGGTGT	2879
Oy Dp	793	ATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAGGTGT	852
ογ	853	ACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCAT	12
QQ	2940	A	2999
δ ξ	- 0	GACTGTACGAATATTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAGGA	972
an o	0 (5	3059
P P	3060	GCCCAGAGAGCTGCTCCTGAGGAGAGCCCAGAATGTCACTGGGCTTCTACGAAAGCA	1032
δy	1033	GGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAG	0.9
QQ	3120	GGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTCCACTCGCTGACTGGCAGAG	17
Qy Db	1093	AAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGA 	1152
οy	1153		5
Dp	3240	CTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCT	7 6
OY Dh	1213		27
3 3	1 6	IGACICICICCAAGAICACCICGAGAAAGTCAAGGCACTICGAGGAGAAATTGCGCC	3359
g K	3360	*CTGAAAGAAGAGGGGGGGGCAGGCAAGGCTTGCCGGGGTTACCACTTTGGGCAT :	1332 3419
δy	1333	TCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCT	39
qq	3420		4.7
οy	1393	CACAGGGACTITGG	45
qq	3480	SAAGCCCACAGGGACTTTGGTCC	3539
λo	45	AGCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGCCATCTCGCC 1	.512
a a	540	CACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGAGCCATCTCGC	1599
OY Pr	513	AAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACATTGCTCGGACCATCCCAA 1	572
<u> </u>	900	CCTACTATATCAACCACGAGACTCAAACAACTTGCTGGGACCATC	629
<u>}</u> {	2/3	AATGACAGAGCTCTACCAGTCTTTAGCTGACTGAATAATGTCAGATTCTCAGCTTATAG 1	.632
a ;	099	TCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTA	719
οy	1633	GACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTC 1	692

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteline-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
1693 AGCTGCATGTGATGCCTTGGACCAGCACCACCTCAAGCAAAATGACCAGCCCATGGATAT 1752
                                                                1753 CCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAAA 1812
                                                                                                                                                                                            New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene.
                                                                                                                               3840 CCTGCAGATTATTAATTGTTTGACCACTATTATGACCGCCTGGAGCAAGAGCACAACAA 3899
                                                                                                                                                                          1813 TTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAACTGGCTGCAATGTTATGA 1872
                                                                                                                                                                                                                                       1873 TACGGGACGAACAGGGAGGATCCGTGTCCTGTTTTAAAACTGGCATCATTTCCCTGTG 1932
                                                                                                                                                                                                                                                           3960 TACGGGACGAACAGGAGGAGCATCCTGTCTTTTAAAACTGGCATCATTTCCCTGTG 4019
                                                                                                                                                                                                                                                                                                        1993 ATTTTGTGACCAGCCAGGCTGGGCCTCCTTCTGCATGATTCTATCCAA 2041
                                                                                                                                                                                                                                                                                                                                                                                         4080 ATTTGTGACCAGCGCAGGCTGCCTCCTCTGCATGATTCTATCCAA 4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adeno-associated virus vector plasmid, AAV-MCK-3447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 65-66; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD37260 standard; DNA; 4414 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Homo sapiens
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control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Beeker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
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3; 2376 2557 ATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAGAAAAGAAAAAAGCAATCCAT 2616 2437 CCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 2496 2497 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTT 2556 2017 AACTGAAGTACAAGAGCAGATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 2076 1777 IGAAGIAAACCIGGACCGTIATCAAACAGCITIAGAAGAAGIATIAICGIGGCITCTIIC 1836 099 GAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAA 840 841 GCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCAT 900 600 901 GAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAA 960 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACAG 720 181 CCAGITICAIACICAIGAGGGTACAIGAIGGAITIGACAGCCCAICAGGGCCGGGIIGG 240 TAATATICTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAAATGGATCTCCAGAATCAGAAACT 420 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAGA 480 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180 63; Gaps 1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60 TGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAAGGTATTGGG 721 TTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGGCTACAGCT Query Match
Best Local Similarity 87.6%; Score 1581; DB 24; Length 4414;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 190; Indels 63; Sequence 4414 BP; 1255 A; 1075 C; 1086 G; 998 T; 0 other; 2257 661 2377 781 541 601 301 361 421 61

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	1 ACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAG	3 AATAAGTCAGTGACCCAGAAGACGGAAGCATGGCTGGA	1 TCTACGAAAGCAGGCTGAGGAGGTCAAT	1 IGACIGGCAGAAAAAAAAGAIGAGACCCTIGAAAGACTCC	1 GGATGAGCTGGACCTCAGCTGGACTGACTGATCAAGGGATCCTGGCAGCCCG	AAGCTGAGGTGATCAAGGGATCCTGGCAGCCG		GGCGATCTCCTCATTGACTCTCTCTAGGCGCGACCTCAGAGATCGCTGGCTG	AATGACCTTGCTCGCCAGCTTA	TAAC IIII TAAC	1 ATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCAAC	4	41 GGACTTTGGTCCAGCATCTCAGCACTTTCTTTCCACGTCTGTCCAGGGTCCCTGGGAGAG 	1 AGCCATCTCGCCAAACAAAGTGCCC	CAAACAAAGTGCCCTACTATTCAACCACGAGACTCAAACAACTTGCT	61 GGACCATCCCAAAATGACAGAGCTC 	1. GORGOTH PARGACTECCT TO GRAPACT COGA A GALGE CAGA A GGCCCTTTGCATC	1 1	81 CTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGACCA	34 CTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGACC	41 GCCCAIGGATAICCIGCAGATATAATIGTTTGACCACTATTATGACCGCCTGGAGCA	94 GCCCATGGATATCCTGCAGATTATTAATTGTTTTGACCACTATTTATGACCGCCTGGAGC	0 1	04 ACAGCACACAACAACAACAACAACAACAACAACAACAACA	, -	21 CATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAGCAAG		81 AAGTTCAACAGGATTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGATTCTATCC
261	96	266	102	0 1	114	279	O O	126	29.	133	'n	0	14.		31	3.2	2 -	32	16	33	17	33		4 6		19		19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4,
                                                                                                                                                                                                                                                                                                                                                             Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
3634 AAGIICAACAGGAITIIGIGACCAGGGAGGCIGGGCCICCIICIGCAIGAITCIAICCA 3693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IGAAGTAAACCIGGACCGITAICAAACAGCTITAGAAGAAGIAITATCGIGGCITCTTIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Gaps
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87.6%; Pred. No. 0;
tive 0; Mismatches 190; Indels 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3446 BP; 1074 A; 766 C; 787 G; 819 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 53-54; 71pp; English.
                                                                                                                                                                                                                                                                                                                       Human dystrophin minigene delta3447.
                                                                                                                                                                                                                                                                                                                                                                                                           Becker muscular dystrophy; ds.
                                                                                                                                                                                          AAD37242 standard; DNA; 3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-2001; 2001WO-US13677.
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                                                                                                                                                                                                                                                                           21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 1787; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-049342/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200183695-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                           2041 A 2041
                                                                                      3694 A 3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-2001.
                                                                                                                                                                                                                                     AAD37242;
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                                                                                                                                                   RESULT 9
                                                                                                                                                                       AAD37242
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1080 IGCTGAGGACACATIGCAAGCACAAGGAGAGATTICTAATGATGTGGAAGTGGTGAAAGA 1139
                                                                             181 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                      241 TAATAITCTACAATIGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                                                                                                                         421 GAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAAGAAGAAAAAGGAAAGA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAAAAAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1679 CCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 TGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAAGAACAACTTAAGGTATTGGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1739 AAAAGAAGATGCAGTGAACAAGATTCACACAGCTGGCTTTAAAGATCAAAATGAAATGTT 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1799 ATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAGAAAAAGAAAAAAGCAATCCAT 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1859 GGGCAAACTGTA-----TTCACTCAAACAAGATCTTTCAACTGAAG 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             961 ACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGGCCCAGAATGTCACTCGGCT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACAG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 721 TTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGGCTACAGCT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 GAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    841 GCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCAT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1021 TCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTCCGC 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1943 -----TAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAA------ 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1081 TGACTGGCAGAGAAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCAC 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1201 GGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 GAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAA 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2036 GGATGAGCTCGAGCTCCAGCCCCAAGCTGAGGTCAAGGGATCCTGGCAGCCCGT
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1921 CATITCCCIGIGIAAAGCACAITIGGAAGACAAGTACAGAIACCITITCAAGCAAGIGGC 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2696 AGAGCACAACAATTTGGTCAACGTCCCTCCTGCGTGGATATGTGTCTGAACTGGCTGCT 2755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1861 GAATGTTTATGATACGGGACGAACAGGGAGCATCCGTGTCCTGTCTTTTAAAACTGGCAT 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1741 GCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGCA 1800
                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAACTGGCTGCT 1860
                                                                                                                                                                                                                                                           1561 GGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATT 1620
                                                                                                                                                                                                                                                                        2456 GGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAATGTCAGATT 2515
                                                                                                                                                                                                                                                                                                         CICAGCITATAGGACIGCCAIGAAACICCGAAGACIGCAGAAGGCCCCITIGCTIGGAICI 1680
                                                                                                                                                                                                                                                                                                                     2516 CTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGATCT 2575
                                                                                                                                                                 1441 GGACTTIGGICCAGCAICTCAGCACTTICCITCCACGICTGCCAGGGICCCTGGGAGAG 1500
                                                                                                                                                                             1501 AGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACAACTTGCTG 1560
                                                                                                                                                                                                                           1381 ATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAG 1440
                                                                                                                             2276 ATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGCAGCTGCATGAAGCCACCACAG 2335
2096 GGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGG 2155
                       Human dystrophin minigene delta3990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD37234 standard; DNA; 3999 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Becker muscular dystrophy; ds.
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H and H4 domains and cyateine-rich domains of dystrophin or utrophin genes. The domains and cyateine-rich domains of dystrophin or utrophin genes. The comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene dalta3990 containing nucleotides 1-1668 (N-terminus, H1 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1320 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TGCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTTCTTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCCTTCACAGGATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 489; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24; Length 3999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3999 BP; 1223 A; 907 C; 933 G; 936 T; 0 other;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.6%; Score 1542;
80.7%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                               Example 1; Page 46-47; 71pp; English.
                                                                                    27-APR-2001; 2001WO-US13677
                                                                                                                 28-APR-2000; 2000US-200777P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                            WPI; 2002-049342/06
                                                                                                                                                                                                                                                                                          dystrophin gene -
                                                                                                                                                  (XIAO/) XIAO X.
                          WO200183695-A2
Homo sapiens
                                                        08-NOV-2001.
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ò	48	CTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 540
QQ	144	. 4
QY DP	541	AGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTCACTCA
οy	601	TGATGAATCTAGTGGAGATCACGCAACTGCTTGCTTTGCTTTTTTTT
QQ	1560	
Qγ	661	AGATCGATCGGCAAACATCTGTAGATGGACAGACGCGCTGGGTTCTTTTTTACAACA717
QQ	1620	AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACCA 1679
Óγ	718	214
QQ	1680	GCCTGACCTAGCTCCTGGACTGACCACTATTGGAGCCTCTCCTACTCAGACTGTTACTCT
δ	718	717
qq	1740	GGTGACACAACCTGTGGTTACTAAGGAAACTGCCATCTCCAAAACTAGAAATGCCATCTTC 1
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g :	0 (SCTACAGCTGAAAGATGAATTAAGCCGGCAGGCACCTATTGGAGGCGACTTTCCAGC 2279
<u></u>		AGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACC 891
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2580 AGAGGCCACGGATGAGCTGGAGCTCAAGCTGGGCCAAGCTGAGGTGATCATGAGGGATCCTG 2639
1072 GCACTCCGCTGACTGGCAGAAAAAAAAAGACCCTTGAAAGACTCCAGGAACTTCA 1131
                                                   1132 AGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTG 1191
                                                                                                                                                 2699
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                                                                                                                                                                                                                                                                      1372 GAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGA 1431
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1612 TGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTG 1671
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RESULT 11 AAD37256

AAD37256 standard; DNA; 4966 BP.

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a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectini gene, H and H4 domains and cysteine-rich domains of dystrophin or utrophin gene, H and H4 invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV dystrophy (BMD) in a mammalian subject. The present sequence is AAV dystrophy (BMD) in a mammalian subject. The present sequence is AAV dystrophy (BMD) in a mammalian subject and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 IGCTGAGGACACATTGCAAGCACAAGGAGATTTTCTAATGATGTGGAAGTGGTGAAAGA 180
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                                                                                                        Human; dystrophin minigene; muscular; gene therapy; utrophin; spect:
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
Becker muscular dystrophy; ds.
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                                                                      Adeno-associated virus vector plasmid, AAV-MCK-delta3990
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Best Local Similarity 80.7%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatche
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                                          21-AUG-2002 (first entry)
                                                                                                                                                                                                                     Chimeric - Unidentified
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1957 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 2016

241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300

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181 CCAGTITCATACTCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGG 240

Gaps

0; Indels 489; DB 24; Length 4966;

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2857 TAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTT 2916
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4177 GCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGA 4236

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                                                         952 ACTAGAGAAACTCTACCAGGAGCCCAGAGGTGCCTCCTGAGGAGAGAGGCCCAGAATGT 1011
                                                                       3157 ACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGT 3216
                                                                                                                  CACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCT 1071
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a cytomegalovirus (CMV) promoter and a small polyA signal sequence.
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                                                                                                                                                                                                                                                       Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
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                                                                                                                                                                                                                    Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3990.
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75.6%; Score 1542; DB 24; Length 4990;
Best Local Similarity 80.7%; Pred. No. 0;
Matches 2041; Conservative 0; Mismatches 0: Indele 400.
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                                                                                                                 AAD37262 standard; DNA; 4990 BP.
                                                                                                                                                                                                                                                                                                                                            Chimeric - Cytomegalovirus. Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2001; 2001WO-US13677
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2032 TTCTATCCAA 2041
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200	2401 AGAICGAIGGGCARACAICTGIRGIRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	717
5 6	2461 GCCTGACCTAGCTCCTGGACTGACCACTATTGGAGCCTCTCCTACT	CAGACIGITACICI	2520
3	718	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	717
5 6	/IO / COMESTANCINAGENANCTECCATCTCCAAACTAGE	AAATGCCATCTTC	2580
3 3	TACA	7 7	717
ž a	2581 CTTGATGTTGGAGGTACCTACTCATAGATTACTGCAACAGTTCCCC	CTGGACCTGGAAAA	2640
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Dp	Db 2881 TAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTT	CATTAGGICCCATIT	2940

GCAGGAACTTCTGGTGTG 771 	rggaggcgactttccagc 83 	ATT(ATT(AGAGCAGCCTTTGGAAGG 951	NGGAGAGCCCAGAATGT 1 	agtgggaaaattgaacct 107 	SACTCCAGGAACTT 	AGGTGATCAAGGGATCCTG 11 	ACCTCGAGAAAGTCAAGGC 129	GTCAATGACCTTGCTCG 13 	TCAGCACTCTGGAAGACCT 1371	GCTGCATGA 14 GCTGCATGA 36	4 7	ACGAGACTCAAAC 15 acgagactcaaac 37	CTGACCTGAATAA 1	STTTAGCTGACCTGAATAA 384 SacrecagaaggcctTTG 167	3 390	GACCAGCACAACCTCA 	TTGACCACTATTTATGACCG 17	TTGACCACTATTTATGACC
CTGCACCTTTCTCT	GCTGAAAGATGATGAATTAAGCCGGCAGGCACCTA 	GCAGAACGATGTACATAGGGCCTTCAAGAGGG 	ATGAGTACTCTTGAGACTGTACGAATATTTCTGA	SAACTCTACCAGGAGCCCAGAGAGCTGCTCCTG	SCTICTACGAAAGCAGGCTGAGGAGGAGTCAATACT SCTICTACGAAAGCAGGCTGAGGAGGTCAATACT SCTICTACAAAGCAGGCTGAGGAGGTCAATACT	CGCTGACTGCCAGAAAATAGATGAGACCCTT CGCTGACTGCCAGAAAATAGATGAGACCCTT CGCTGACTGGCAGAAAAATAGATGAGAGACCCTT	ACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTG 	CGGIGGGCGATCTCGTCATTGACTCTCTCCAAGATC	GAGGAGAAATTGGGGCGTTGAAAGAGAACGGGGGCGGGGGGGG	TTACCACTTTGGGCATTC	ACCAGATGGAAGCTTCTGCAGGTGGCCGT	CAGAGACTTTGGTCCAGCATCTCAGCA	GAGAGGCCATCTCGCCAAACAAAGTGCC	GGAGAGCCATCTCGCCAAAATGACAGGGGGGGGGGGGGG	rgcTgggaccaTcccaaaaTgacagaggTcTacc	PATAGGACTGCCATGAAACTCC 	SGATCTCTTGAGCCTGTCAGCTGCATGT	GGACCAGCCCATGGATATCCTGCAGATTATTAATTG	ACCAGCCCATGGATATCCTGCAGATTATTATTG
718	72 GCTA 	32 AGTT 	892 TGTA	952 ACT	12 CF	072 GCAC 1111 301 GCAC	132 AGAG 111 111	192	421 GC 252 AC 11 481 AC	312 CC	372	3501 GAAG 1432 AGC 111	492 CTG	AAC	1 AAC	1612 TGT(3841 TGT	672 C	3901 CT	3961 AAATC
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CIGGCTGCTGAATGTTAATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTAA 1911
                                                                                     4081 CTGGCTGCTGAATGTTATGATACGGACGACGAGGAGGATCCGTGTCCTGTCTTTAA 4140
                                                                                                                        AACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAA 1971
                                                                                                                                                       AACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAA 4200
                                                                                                                                                                                                            GCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGA 2031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human dystrophin minigene delta4173.
                                                                                                                                                                                                                                                                                                                                                                                  AAD37230 standard; DNA; 4182 BP
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                                                                                                                                                                                                                                                                                              4261 TTCTATCCAA 4270
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.

WO200183695-A2.

08-NOV-2001.

27-APR-2001; 2001WO-US13677.

28-APR-2000; 2000US-200777P.

(XIAO/) XIAO X.

WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a

dystrophin gene

Example 1; Page 43-44; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAN) comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta4173 containing nucleotides 1-1992 (N-terminus, hinge H1 and rods R1, R2 and R3), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

Sequence 4182 BP; 1309 A; 927 C; 970 G; 976 T; 0 other;

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Ä
                                                             121 TCCTGAGGACACATTGCAAGCACAAGGAGATTTCTAATGATGTGGAAGTGGTGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                    1680 CCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGA 1739
                                                                                                                                                                                                                                   241 TAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGA 300
                                                                                                                                                                                                                                                                               301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1740 AAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTT 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1860 GGGCAAACTGTATTCACTCAAACAAGATCTTTCAACACTGAAGAATAAGTCAGTGAC 1919
                                                                                                                                                                                                                                                                                                                                                                            481 GCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 AGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTCACATCACATGGTGGTGGTAGT 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 AGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGA--- 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1920 CCAGAAGACGGAAGCAIGGCIGGAIAACITIGCCCGGIGTIGGGAIAATITAGICCAAAA 1979
                                             1 TCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCATTTGGCAGTTCATTGATGGAGAG 60
                                                                                                                                                                                     181 CCAGITICATACTCATGAGGGGTACATGATGGATITGACAGCCCATCAGGGCCGGGTTGG
                                                                                                                                                                                                                                                                                                                              361 TAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACT
                             Indels 672;
       Length 4182;
       DB 24;
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  66.6%; Score 1359; D
75.2%; Pred. No. 0;
Live 0; Mismatches
                       Matches 2041; Conservative
Query Match
Best Local Similarity
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qq	1980	0	
οy	718	717	
g	2040	AAAGTTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTAC 2099	
οy	718	717	
QQ	2100	ccgtaaggaaaggctcctagaagactccaagggagtaaaagagctgatgaaacaatggca 2159	
οy	718	717	
Dp	2160	AGACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAG 2219	
οy	718	717	
qq	2220	CCAAAAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTT 2279	
δý	718	717	
Dp	2280	GGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCCA 2339	
δ	71	1 0	
<u>a</u> :	2340	TIGGARAGCCAGIICIGACCAGIGGARAGCGICCIGCCACITACCAGIGGAGGCGACTTTCC	
3 8			
ò	82	GCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAACAGGGAATTGAAAACT	
qq	2460	I I I	
yo d	889	ACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGA 948 	
3 8	94	SACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGA	
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Οý	1009	90	
Dp	2640	GTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAA 269	
Qy Ph	1069	CCTGCACTCCGCTGACTGCCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACT 1128 	
3 8	, ,	CARGAGGGGAAGGAGGAGGAGGAGGAGGAGGAAGCTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGAAGGTAAGAAG	
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δy	1189	CTGGCAGCCGTGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAAGTCACA	
qq	2820	CIGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCTCAAGATCACCTCGAGAAAGT	
οy	24	GGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGC 130	
QQ	2880	GGCACTTCGAGGAGAATTGCGCCTCTGAAAGAAAACGTGAGCCACGTCAATGACCTTGC	
ò	30	TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGA 1388	
QQ	2940	TCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCTGGGCACTCTGGGGAGA	
yo 4	1369	CCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCGAGGCAGCTGGCAGTTGGAGTGGCTGCTGAGTGGCCGGTCGAGGACCGAGTTCAGGCAGCTGGAGGTGGCCGTGGAGGACCGAGTCAGGAACGAAC	
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                  1909 TAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTT 1968
                                                                                                                                                                                                                                                                                                                                    3360 GCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTATGA 3419
                                                                                                                                                                                                                                                                                 1849 GAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTTT 1908
                                                                                                                                                                                                                                                                                           3060 IGAAGCCCACAGGGACTITGGTCCAGCATCTCAGCACTITCTTTCCACGTCTGTCCAGGG 3119
                    1609 TAATGICAGATICICAGCITATAGGACIGCCATGAAACICCGAAGACIGCAGAAGGCCCI 1668
                                                                                                                    1669 TTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAA 1728
                                                                                                                                                              1729 GCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGA 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human dystrophin rod, hinge and CR domain regions encoding DNA #1.
                                                                1549 AACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD37232 standard; DNA; 2169 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-2001; 2001WO-US13677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           3660 TGATTCTATCCAA 3672
                                                                                                                                                                                                                                                                                                                                                                                                                   2029 TGATTCTATCCAA 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-049342/06.
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                     dystrophin gene
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Example 1; Page 45-46; 71pp; English.

a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) element. The dystrophin minigene operably linked to an expression control control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy not bus fragment encoding rods R22, R23 and R24, hinge H4 and present invention relates to an isolated nucleotide sequence encoding CR domain regions.

Sequence 2169 BP; 623 A; 529 C; 524 G; 493 T; 0 other;

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0;
                                                                                                                                                                                                           CITIGGAAGGACIAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAG 1001
                                                                                                                                                                                                                                                   1002 CCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAA 1061
                                                                                                                                                                                                                                                                                            1062 AATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCC 1121
                                                                                                                                                                                                                                                                                                                                     1122 AGGAACTICAAGAGGCCACGGAIGAGCIGGACCICAAGCIGCGCCAAGCIGAGGIGAICA 1181
                                                                                                                                                                                                                                                                                                                                                                              1182 AGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGA 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 GGGTTCTTTTACAAGACAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAAC 761
                                                   242 AAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAGGTGAGCCACGTCAATG 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1302 ACCITGCICGCCAGCITACCACITIGGGCAITCAGCICICACCGIAIAACCICAGCACIC 1361
                                                                                822 ACTITCCAGCAGTICAGAAGCAGAACGAIGTACAIAGGGGCCTICAAGAGGGAATIGAAAA 881
                                                                                                                                    CIAAAGAACCIGIAAATCAIGAGIACICIIGAGACIGIACGAAIAIIIICIGACAGAGCAGC 941
                                                                                                                                                                             Gaps
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                         0;
                       7; Indels
65.1%; Score 1328.8;
99.5%; Pred. No. 0;
tive 0; Mismatches
        Best_Local Similarity 99.5
Matches 1333; Conservative
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Xiao X;

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1542 AGACTCAAACATGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTG 1601
                                                                                               1602 ACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGA 1661
                                                                                                                                        Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                      1662 AGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACA 1721
                                                                                                                                                                                                                                                           1782 ITTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATA 1841
                                                                                                                                                                                                                                                                                                     1842 TGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAAGGGAGGATCCGTGTCC 1901
                                                                                                                                                                                                                                                                                                                 1902 TGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGAT 1961
                                                                                                                                                                                                                                                                                                                                                                                                    1482 TCCAGGGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG
                                                                                                                                                                                                                 ACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTA
                                                                                                                                                                                                                                                                                                                                                                                         1962 ACCITITCAAGCAAGTGGCAAGTICAACAGGATTITGIGACCAGCGCAGGCTGGGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human dystrophin rod, hinge and CR domain regions encoding DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTGCATGATTCTATCCAA 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1653 TTCTGCATGATTCTATCCAA 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD37241 standard; DNA; 1821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, and repeats, H1 and H4 domains and a cysteine rich domain of a dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin DNA fragment encoding rods R23 and R24, hinge H4 and CR Example 1; Page 52-53; 71pp; English. WPI; 2002-049342/06. dystrophin gene

Sequence 1821 BP; 506 A; 451 C; 447 G; 417 T; 0 other;

domain regions.

Gaps . 0 DB 24; Length 1821; Indels 0 0; Mismatches 64.9%; Score 1324; I 100.0%; Pred. No. 0; Matches 1324; Conservative Best Local Similarity Query Match

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718 CAGTICIGACCAGIGGAAGCGICIGCACCTITCICIGCAGGAACIICIGGIGIGGCIACA 777 778 GCTGAAAGATGATTAAATTAAGCCGGCAGGCACTATTGGAGGCGACTTTCCAGCAGTTCA 837 ò ò

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GAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGAGCCCAGAATGTCACTCG 1017 898 CATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGA 928 GCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTC 1077 360 GCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTGCACTC 301 Op õ

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CGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTCG 1257 CACGGATGAGCTGGACCTCCAAGCTGCGCGAGGTGATCAAGGGATCCTGGCAGCC 480 421

1258 AGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCT 1317 541 AGGAGAAATTGCGCCTCTGAAAGAAAGGTGAGCCACGTCAATGACCTTGCTCGCCAGCT

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1858 GCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTTAAAACTGG 1917 1918 CATCATITCCCIGIGIAAAGCACAIIIGGAAGACAAGIACAGAIACCTITICAAGCAAGI 1977 1738 CCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGA 1797 1798 GCAAGAGCACAACAATTTGGTCAACGTCCCTCTGTGGGATATGTGTCTGAACTGGCT 1857 1438 CAGGGACTTTGGTCCAGCATCTCAGCACTTTTTTTCCACGTCTGTCCAGGGTCCCTGGGA 1497 GAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACAACTTG 1557 CIGGGACCATCCCAAAATGACAGAGCTCTAACCAGTCTTTAGCTGACCTGAATAATGTCAG 1617 1618 ATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGA 1677 1678 TCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGA 1737 1378 CAGAIGGAAGCIICIGCAGGIGGCCGICGAGGACCGAGICAGGCAGCIGCAIGAAGCCCA 1437 841 CIGGGACCAICCCAAAATGACAGAGCICIACCAGICITIAGCIGACCIGAATAAIGICAG 900 2038 CCAA 2041 1321 CCAA 1324 1498 1558 ò q Óλ Dp qq ò Оp òγ g δλ g

Search completed: April 25, 2003, 08:45:30 . 379.763 secs Job time

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449 22.0 704 10 BB610411 428.6 21.0 854 9 AI196693 3410.4 20.1 599 10 BB66688 380.2 18.7 423 9 AA60476 380.2 18.6 684 9 AL641565 368.6 18.1 633 9 AL672616 329 16.1 532 13 BD734408 315.4 15.2 532 13 BD73615 315.4 15.2 541 13 BD746721 303 14.8 597 9 AL121550 297.8 14.6 655 10 BE231408 297.8 14.6 655 10 BE201973 297.8 14.6 655 10 BE201973 207.8 14.6 655 10 BE201973 255.4 12.5 772 13 BD76562 265.8 13.0 784 12 BC212445 255.4 12.5 772 13 BD736168 256.4 10.1 733 12 BF14477 206.4 10.1 733 12 BF14477 206.4 10.1 479 14 BG30404 10.1 479 14 BG30404 10.1 479 14 BB21285 1184.8 9.0 475 12 BG27463 115.4 7.5 481 10 BE57463 115.4 7.5 481 10 BE57463 115.4 7.5 481 10 BE57463 1142.4 7.0 1002 12 BF298394 142.2 7.0 426 14 BQ319056	AL556247 Homon sapiens Eukaryota Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Primates; Catarrhini; Homini; Li, Wa B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedax - France BP 191 91006 EVRY cedax - France Email: seqref@genoscope.cns.fr, Web: www.genoscoperion/Qualifiers Location/Qualifiers //organism="Momo sapiens" //db_xref="taxon:9060" //clone="CSOBKON1817" //clone="CSOBKON1817" //clone="CSOBKON1817" //clone="CSOBKON1817" //clone="Libraries" //db_xref="LTI_NFL006_PL2" //tissue_type="placenta" //note="Vector: pONVSPORT 6; Site_1: Notiwas primer was primed with a NotI-oligo(dT) primer
s/sec 1 10 10 11 11 11 11 11 11 11	RESULT 1 AL55647 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT COMMENT COMMENT FEATURES SOURCE AUT TOTAL JOHN SAPP SOURCE SAPP 1984 USCU

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National Eye Institute

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Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of human retina for the NELBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), (2002) in press
Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear EST 15-JUL-2002
enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URA. : http://fulllength.invitrogen.com"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 4...
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505; Conservative
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/atb_inst__enuniatus
/note="Organ: Eye; Vector: pSPORTI; Neural retina tissue
/note="Organ: Eye; Vector: pSPORTI; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORTI vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adapter [5'-pGACTAGTTCTAGATCGCGAGGGCGCCCC(T)15-3'
]. EST analyzis was performed on the unamplified library
at the NIH Intranural Sequencing Center (NISC)."
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                                                                                                                                                                                                       /clone_lib="Human Retina cDNA (Un-normalized, unamplified
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100.0%; Pred. No. 1.8e-109;
6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452
Fax: 301 496 0078
                                                        Email: graeme@helix.nih.gov
Plate: 23 row: g column: 04
Seg primer: M13RP1 reverse primer (ABI).
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100.0%; Mismatches
                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="EMDH10B"
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                                                EST 08-MAY-2001
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                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Butheria; Butheria; Lo 770; Primates; Catarrhini; Hominidae; Homo. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                 BG719710
602690430F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4822807 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: testis, Vector: pBluescriptR (modified bBluescript KS+): Site_1: BamH1: Site_2: Salr.xhor (gtcg.): Oligo-dT primed using primer 5 'TTTTTTTTTTTTTTVTVN'3' size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1537 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTT 1596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1717 GCACAA--CCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTG 1774
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                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM10731 row: 1 column: 08
High quality sequence stop: 767.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIH_MGC_97"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4822807"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                       BG719710.1 GI:13998897
                                                                                                                                                                                                                                                                  Unpublished (1999)
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Best Local Similarity 98.28
Matches 498; Conservative
                                                                       mRNA sequence.
BG719710
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RESULT 3
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Homo sapiens, dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272, clone IMAGE:3029414, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   through the I.M.A.G.E. Consortium/LLNL at: http://image.lnnl.gov
Series: IRAL Plate: 10 Row: j Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5032280
This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-JUN-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                           1895 CGTGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAG 1954
                                                                                                                                                                               1955 TACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTG 2014
0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
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/db_xref="LocusID:1756"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                      2015 GGCCTCCTTCTGCATGATTCTATCCAA 2041
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299 c 328 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinaqawa,A., Shiraki,T., Soqabe,Y., Suzuki,H., Tagami,M., and Hayashizaki,Y., Tanaka,T., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Rawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehlro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Haytsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RİKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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                                                                                                                                                                                                                                                                                                                 1329 AACTGAAGTACAAGAGCAGATGAAATCTCCTAAATTCAAGATGGGAATGCTCAGGGTAGC 1388
                                                                                               1029 ICCTICACAGCAITIGGAAGCICCIGAAGACAAGICAITIGGCAGIICAIIGAIGGAGA 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGC 360
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                                                                                                                                                                                                                                                                                       240
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                                                                                                                                                                         121 TGCTGAGGACACATTGCAAGCACACGAGAGATTTCTAATGATGTGGGAAGTGGTGAAAGA 180
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BB629984 RIKEN full-length enriched, adult female vagina Mus
musculus cDNA clone 9930028B14 5', mRNA sequence.
                                                                                                                                                                                                                                                                                    181 CCAGTITCATACTCATGAGGGGTACATGGATTTGACAGCCCCATCAGGGCCGGGTTGG
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
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VERSION KEYWORDS

TITLE COMMENT

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                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) ananaka,I., Kiyosawa,H., Kondo,S., Salto,T., Shinagawa,A., Aizawa Yamanaka,I., Kiyosawa,H., Kondo,S., Salto,T., Shinagawa,A., Aizawa Yamanaka,I., Hayasahazaki,Y. and Hayashazaki,Y. Maphing of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Planc. Genomics 2 pre, L72-186 (2001 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Konno, H., Fukunishi, Y. and Hayashizaki, Y. and Hayashizaki, Y. computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTVN 3'], CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: Sall; Site_2: BamH; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1717 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1776
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0; Mismatches 32
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/db_xref="taxon:10090"
/clone="9930028B14"
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/dev_stage="adult"
/lab_host="DH10B"
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1. .652
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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. and Hayashizaki, B. and Hayashizaki, B. and Hayashizaki, G. and Hayashizaki, G. and Hayashizaki, G. and Hayashizaki, G. and J. a
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/db_xref="taxon:10090"
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male hippocampus cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
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Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:290010C03:dystrophin, muscular dystrophy,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1897 IGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1956
                                                                                                                                                                         1957 CAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGAGGCTGGG 2016
                                             Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
                                                                                                                                                                                                                                                                                                                                                  2017 CCTCCTTCTGCATGATTCTATCCAA 2041
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Aizawa, K., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Handa, T., Hori, F., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kaya, T., Kato, H., Kadai, Y., Kouda, M., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Saski, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tagami, M., Tagama, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamanura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Vokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, WRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/db_xref="G1:12850900"
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VPLCYDMCLNWLLNVYDTGRTGRIPVLFSKTGIISCKAHLEDKYRYLFRQVASSTGF
CDQRRLGLLHDSTQIPROLGEVASFGGSNIEDESVRSCFOFANNKPEIEAALFLDWMR
LEPQSMYWLPVLHRVAAAETAKHQAKCNICKECPIIGFRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 704)

Arakawa T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishli, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Chara, M., Sahi, Y., Sahi, Y., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Alakawa, T., et al. 2001)
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Contract: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
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                                                                                             1537 CCACGAGACTCAAACAACTTGGTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1596
                                                                                                                                                                                                   ACCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 1656
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                                                                                                                                                                                                                                                                                                                                                                                                                           204 AGCTGACCTGAATAATGTCAGGTTCTCCGCGTATAGGACTGCCATGAAGGTCAGAAGGCT 263
                                                                                                                                            144 CCACGAGACCCAAACCACTTGTTGGGACCACCCCAAAATGACAGAGCTCTACCAGTCTTT 203
                                                 0; Gaps
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  DB 11; Length 2135;
                                                    Indels
Query Match 22.2%; Score 453.8; DB 1 Best Local Similarity 93.7%; Pred. No. 1.5e-99; Matches 473; Conservative 0; Mismatches 32
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BB610411.1 GI:16451938
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COMMENT

TITLE

VERSION

q

SOURCE

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/tissue_type="pancreas"
/dev_stage="10 day old"
/note="vector: pspoRTi" site_1: Sall; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos extraembryonic part of E7.5 embryos ovary cDNA library. Average libert size 1.5 kb. All source libraries are cloned unidirectionally with oligo(dT
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinaqawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                                                                                                                                                                                               sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patterns during preimplantation mouse develolpment, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )-Not primers. References include: (1) Genome wide expression profilling of mid-gestation placenta and embryc using a 15,000 mcuse developmental cDNA microarray, 2000, proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RIKEN full-length enriched, 10 day old male
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197 AGCTGACCTGAATAATGTCAGGTTCTCCGCGTATAGGACTGCCATGAAGCTTCAGAAGGCT 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810074E05"
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1. .704
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Ω δ ò qq qq Ω g δ g ò d

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AI196693 854 bp mRNA linear EST 14-OCT-1998 ui53e10.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1886154 5' similar to 9b:M18533 DYSTROPHIN (HUMAN); gb:M68859 Mouse dystrophin mRNA, exons 1-7 and complete cds (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 854)
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/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                                          1717 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1776
                                                                                                                               1777 CACTAITIAIGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGGGT 1836
                                                                                                                                                                                                                       1837 GGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 1896
                                                                                                                                                                                                                                                                                                            1897 TGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1956
                                                                                                                                                                                                                                                                                                                                                                                                 257 CCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCCGCTGCATGTGATGCCCTGGACCA 316
                                                                  This clone is available royalty-free through LLNL; contact the IMAGE CORSORTIUM (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Sugano mouse liver mlia"
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Location/Qualifiers
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/clone="IMAGE:1886154"
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MGI:970478
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JOURNAL
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SOURCE

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was primed with an oligo(dT) primer [ATGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Draili adaptor [TGTTGGCCTACTGG], digested and cloned into distinct Draili sites of the pMEIBS-FL3 vector (5' site CACTGTGTG) 3' site CACTGTGTG). XhoI should be used to isolate the cDNA insert. Size selection was constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                 Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACAA."
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Rawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1956 ACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGG 2015
                                                                                                                                                                                                                                                                                                                                                                                                 255 CCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCAGCTGTGATGTCTTGGACC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                      DB 9; Length 854;
                                                                                                                                                                                                                                          3 others
                                                                                                                                                                                                                                                                                                                                            41; Indels
                                                                                                                                                                                                                                                                                               Score 428.6; DB 9
Pred. No. 1.7e-93;
                                                                                                                                                                                                                                          209 t
                                                                                                                                                                                                                                                                                           Query Match
21.0%; Score 428.6;
Best Local Similarity 91.7%; Pred. No. 1.7e
Matches 463; Conservative 0; Mismatches
                                                                                                                                                                                                                                    208 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2016 GCCTCCTTCTGCATGATTCTATCCA 2040
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1657 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA 1716

1597 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT

137 CCACGAGACCCAAACCACTTGTTGGGACCACCCCAAAATGACAGAGCTCTACCAGTCTTT 196

257 CCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCCTGGACCA 316

1717 GCACAACCTCAAGCAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1776

q δλ

g

1777 CACTAITTATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTCTGCGT 1836

1837 GGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCG 1896

Qγ g

1897 IGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1956

1957 CAGATACCITITCAAGCAAGTGGCAAGTTCAACAGGAITT 1996

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RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGGCGCAGATTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 161 c 142 g 150 t
                                                                                                                                                                                                                                                                                                                              Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata.Y., Hayatsu.N., Sugahara.Y., Shibata.K., Itoh
Carninci.P., Shibata.Y., Hayatsu.N., and Hayashizak.Y.
M., Konno,H., Okazaki.Y., Muramatsu.M. and Hayashizak.Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi.K., Fujiwake.S., Inoue.K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                         1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nayacantania Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared With Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="E330026B12"
/clone_lib="RIKEN full-length enriched, 2 days pregnant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="ovary"
/dev_stage="2 days pregnant adult"
/lab_host="DH108"
                                                          RIKEN Mouse ESTS (Arakawa,T., et al. 2001) unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
                                             Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,K., Fukuda,S
Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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/note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week
                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 423)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucabb,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
,T., Waterston,R. and Wilson,R.
WashJ.Merck EST Project 1997
                                                                                                                                        EST 09-JUN-1997
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: estéwatson wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28mils rev2 ET from Amersham
High quality sequence stop: 287.
                                                                                                                                                             zx61e10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:795978 5' similar to gb:M18533 DYSTROPHIN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares.total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH108"
                                                                                                                                                  linear
Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:6039697"
                                                                                                                                                     423 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:795978"
                                                                                                                                                                                                                                                                         AA460476.1 GI:2185222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                  sednence.
                                                                                                                                                        AA460476
                                                                                                                                                                                                                                                    AA460476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                               SOURCE
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1537 CCACGAGACTCAAACAACTTGGTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1596

0; Mismatches

20.1%; 93.3%;

Best Local Similarity 93.3' Matches 429; Conservative

Similarity

Query Match

Score 410.4; DB 10; Length 599; Pred. No. 4.1e-89;

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õ qq q à g δ Q ò g δ a

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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
AL641565 XGC-neurula Silurana tropicalis cDNA clone TNeu012d20 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                 1537 CCACGAGACTCAAAACAACTTGCTGGGACCATCCCAAAATGACAGGGTCTTACCAGTCTTT 1596
                                                                                                                                                                                                                                                                                                                                           1597 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 1656
                                                                                                                                                                                                                                                                                                                                                                                                                      1657 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA 1716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1837 GGATATGTCTCTGAACTGGCTGCTGAAT-GTTTATGATACGGGACGAACAGGGAGGATCC 1895
                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Rogers, J.
                                                                                                                                                                                                    DB 9; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Silurana.

1 (bases 1 to 684)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rog Sanger Xenopus tropicalis EST project 2001 (10_2001)
Contact: Huckle E
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu012d20.sp6
                                                                                                                                                                                           18.7%; Score 381.8; DB 9 99.2%; Pred. No. 3.5e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1896 GTGTCCTGTCTTTAAAACTGGCATCATTTCCCTGTG 1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Silurana tropicalis"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constructed by Aaron M. Zorn.
Location/Qualifiers
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                                                                                                                                                                                                          Best_Local Similarity 99.2%
Matches 394; Conservative
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                                                                                                                                                                                       Query Match
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ACCESSION

KEYWORDS

/ERSION

RFERENCE

JOURNAL

TITLE OMMENT EATURES

RESULT 11

AL641565

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ö
                             /dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pcSl0; Site_1: EccRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pcSl07 with
EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF182065
601804604F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4035505 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 898)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                    1537 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTT 1596
                                                                                                                                                                                                                                                                                                                                          1597 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 1656
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                                                                                                                                                                                                                                                                                       115 CCAIGAGACACAAACCACCTGCTGGGATCATCCCAAAATGACAATATAACCAATCTT 234
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                       DB 9; Length 684;
                                                                                                                                                                                                 18.6%; Score 380.2; DB 9; Length 684.6%; Pred. No. 9.6e-82;
tive 0; Mismatches 78; Indels
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                   /clone_lib="XGC-neurula"
/clone="TNeu012d20"
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BF182065
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/lot-houst Escherichia coli DH10B" /lote="Scherichia coli DH10B" /note="Vector: pC5107; Site_1: EcoR1; Site_2: NotI; cDNA /note="Vector: pC5107; Site_1: EcoR1; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. was oligo dT primed from 5ug of poly A+ RNA from neurula. was oligo dT primed from 10 pc10 y with EcoR1 at the 5' end and NotI at the 3' end."
                               Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Emphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
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                                                                                                                    Zorn, A.M. and Rogers, J.
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Location/Qualifiers
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                                                                                                                                                                                                                                                          Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: INeu143c03.plcSP6
Sequencing primer: PlcSP6
                                                                                                                       Taylor,R., Ashurst,J.L., Croning,M.D.R., 2c
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Silurana tropicalis"
                                                                                                                                                                                                                           Hinxton, Cambridgeshire, CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="TNeu143c03"
/clone_lib="XGC-neurula"
                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="neurula"
                                                                                                                                                                                                                                                    Email: trop@sanger.ac.uk
              western clawed frog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                     /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1774 GACCACTATTTATGACCGCCTGGAGCAAGAGCACAA-CAATTTGGTCAACGTCCCTCTT 1832
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.h column: 02
plate: LLAM9309 row: h column: 02
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Best Local Similarity 92.4%; Pred. No. 2.1e-80;
Matches 471; Conservative 0; Mismatches 32: Indels 7
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                                                                                                                                                                                                                                                                               /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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/clone="IMAGE:4035505"
/clone_lib="NCI_CGAP_Mam5"
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                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                          High quality sequence start: 3
High quality sequence stop: 675.
Location/Qualifiers
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                                                                                                                                                                                                          /strain="C57BL/6J"
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535 CGTCTTATCTTTAAAACTGGTGTAATTTCCCTGTGTAAAGCACATTTGGAAGATAAGTA 594
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Location/Qualifiers
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                                                                                                                                                                                                                                                          BE334408.1 GI:9208184
                                                  1957 CAGATACCTTTTCA 1970
                                                                                 595 CAGATACTTATTCA 608
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                                                                      AL672616 XGC-gastrula Silurana tropicalis cDNA clone TGas054h08 5',
                                                                EST 18-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/note="Vector: pCS107; Site_1: EcoR1; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                           Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                               Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J. Sanger Kanopus tropicalis EST project 2002 Unpublished (2011)
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing primer: P1CSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                      Sanger Xenopus tropicalis EST project 2001
                                                                                                                                                                                                                                                                                                                                                                                                      TROFICALIS_SEQUENCE_ID: TGas054h08.plcsP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TGas054h08"
                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                      Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
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                                                       e08 bp
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                                                                                                                                                                                                                                 Xenopodinae; Silurana.
1 (bases 1 to 608)
                                                                                                                                                            western clawed frog.
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Best Local Similarity 85.09
Matches 369; Conservative
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                                                                                             mRNA sequence.
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                                                       AL672616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Source
                                                                        DEFINITION
                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                JOURNAL
COMMENT
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                                                                                                        ACCESSION
                                                                                                                          VERSION
KEYWORDS
                                     AL672616
LOCUS
                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                 AUTHORS
                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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Dolylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - Ollgo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
        EST 14-JUL-2000
                          ug97g06.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:1550362 5' similar to gb:M68859 Mouse dystrophin mRNA, exons
1-7 and complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                    1 (bases 1 to 532)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapDs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1537 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1597 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 1656
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     linear
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/db_xref="taxon:10090"
/clone='InAGE:1550362"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 16.1%; Score 329; DB 10; Best Local Similarity 93.2%; Pred. No. 2.6e-69; Matches 344; Conservative 0; Mismatches 25;
        mRNA
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
532 bp
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 - Op
- Search completed: April 25, 2003, 17:39:13 Job time : 1950.12 secs

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April 25, 2003, 08:10:12 ; Search time 46.4852 Seconds (Without alignments) 13465.096 Million cell updates/sec
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Patent No. 5180810
Sequence 76, Appl
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Sequence 1, #
Sequence 1, #
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Sequence 22
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-887-534A-22
US-09-007-005-17
US-09-244-796-17
US-09-014-969-14
US-08-630-915A-193
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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US-08-139-937-12
PCT-US93-11310-12
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PCT-US93-07261-10
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US-08-317-844B-3
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US-09-247-155-76
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US-09-092-458-1
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US-08-676-974-5
US-09-098-487-5
                                                                                                                                                                     441362 seqs, 153338381 residues
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PCT-US95-10668-4
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                                                                                               US-09-845-416-12_COPY_960_3000
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US-08-072-610-1
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                                  OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Score Match Length DB
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Maximum DB seq length: 5000
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Sequence 11, Appl
Sequence 13, Appl
Sequence 184, App
Sequence 204, App
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9, Appli
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Sequence 1, Ap
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TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTRARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PatentIn Release #1.0, Version #1.30 APPLICATION NUMBER: US/08/257,073 FILING DATE: 09-JUN-1994 CLASSIFICATION A24 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/075,783 FILING DATE: 11-JUN-1993
                                             US-09-461-697-189
US-09-461-697-187
US-09-461-697-185
US-09-671-950-3
US-09-671-950-3
US-09-671-950-5
US-09-671-950-9
US-09-671-950-11
                                                                                                                                                                                                     US-08-961-527-370
     US-08-857-076-44
US-08-857-076-43
US-09-007-005-3
                                       US-09-244-796-3
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530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                           ALIGNMENTS
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TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 840-3333
TELERAX: (212) 840-0712
TELEX: 42066 CUFTMS
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/852,305-
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08257073
Patent No. 5766597
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
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                                                                                                                                                                                                                                                                                                                                                                                  143
  22704
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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STRANDEDNESS: single
 New York
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US-08-257-073-4
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MOLECULE TYPE:
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US-08-317-844B-3
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APPLICANT: Lewis, Ming
APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                       468 AAATGGAGGAAGAGCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAAC 527
                                                                                                                                                                                                                        2153 AAGAAGAAGAAGAAGAAGAAGAAGAAATAGTACCAGAAAATTTGACAACTGA 2210
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tive 0; Mismatches 209; Indels 0;
2.0%; Score 40.4; DB 1; Length 2223; 51.7%; Pred. No. 0.042; tive 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Birch, Stewart, Kolasch & Birch
: 301 No. 5728810th Washington Street
Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/425,069
19-APR-1995
                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/08425069
; Patent No. 5728810
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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NAME: MULPhy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
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TELEFAX: (703) 205-8050
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LENGTH: 1995 base pairs
TYPE: nucleic acid
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                                             92; Conservative
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HYPOTHETICAL: NO
       Query Match
Best Local Similarity
Matches 92; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Virginia
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CLONE: p6B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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LOCATION:
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US-08-425-069-3
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APPLICANT: Lewis, Randolph V.
APPLICANT: Lewis Randolph V.
APPLICANT: Lewis Ming
APPLICANT: W. Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                  1130 CAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCC 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                           971 TAGGAGGITATGGACCAGGACAACAAGGICCAGGAGGATAIGGACCAGGACAACAAGGIC 1030
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                                                                                                                                                                        1010 GTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAAC 1069
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                                                                                                                                                                                                    830 GCAGTICAGAAGCAGAACGATGIACAIAGGGCCTICAAGAGGGAAITGAAAACIAAAGAA 889
                                         731 GCAGTGCAGCTGCAGCAGCAGCAGGACCTGGACAACAAGGACCCGGAGGATATGGAC 790
                                                                                     890 CCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAA 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: Birch, Stewart, Kolasch & Birch: 301 No. 5989894th Washington Street Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MUTPHY Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08317844B patent No. 5989894 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 241-1300
(703) 241-2848
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy of
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ADDRESSEE: Birch, St
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NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.9%; Score 38.2; DB 6; Length 1131;
Best Local Similarity 45.9%; Pred. No. 0.13;
Matches 130; Conservative 0; Mismatches 153; Indels o.
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Patent No. 5180810

Patent No. 5180810

Patent No. 5180810

Tarachi Kashimoto, Funitaka; Bjorck, Lars

Tarachi Kashimoto, Funitaka; Bjorck, Lars

Tarachi Seguences: 4

CURRENT APPLICATION DATA;

APPLICATION NUMBER: US/07/376,641

FILING DATE: 07-UUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 153; Indels
                                                                                                                                                    Matches 164; Conservative
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                                                                    ; LOCATION: 1.1785
US-08-317-844B-3
IMMEDIATE SOURCE:
                                                  NAME/KEY: CDS
                                                                                                                       Query Match
                                   FEATURE:
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281 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 340
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                                                                                                                                                                                                              APPLICANT: Gomi, Hideyuki,Hozumi, Tatsunobu;Hattori, Shizuo;
Tagawa, Chiaki;Kishimoto, Fumitaka;Bjorck, Lars
TITLE OF INVENTION: PROTEIN H CAPABLE OF BINDING TO IGG
521 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAG 563
                                     397 TTAGAACGTAAATACCAACGAGAAGTAGAAAACGTTATCAAG 439
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APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
TITLE REFERENCE: Green 1999-02-09
CURRENT APPLICATION NUMBER: 05/09/247,155A
CURRENT APPLICATION NUMBER: 06/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/091,563
EARLIER PLING DATE: 1998-08-03
EARLIER PLING DATE: 1998-08-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/096,123
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEO ID NOS: 182
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/376,641
FILLNG DATE: 07-JUL-1989
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
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ORGANISM: Homo sapiens
                                                                                                                                                                                       ; Patent No. 5180810
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1784
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5180810-2
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                                                                                                                                                                                                                                                                                                                                                                                          369 AAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGT 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Patent No. 5210183; PRITHZ, ELISABET; HEDEN, LARS-OLOF TILLE OF INVENTION: PROTEIN ARP, WITH IMMUNGLOBULIN A BINDING ACTIVITY, THE CORRESPONDING VECTORS AND HOSTS, REAGENT KIT AND PHARMACEUTICAL COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.9%; Score 38; DB 4; Length 1394; Best Local Similarity 59.1%; Pred. No. 0.17; Matches 65; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 157; Indels
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                                                                                                                     OTHER INFORMATION: SEG LTLLGLSLILAGL/IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPANY AS LICATION DATA:
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/270,099
FILING DATE: 14-NOV-1988
APPLICATION NUMBER: 186,097
FILING DATE: 25-APR-1988
                                 NAME/KEY: sig_peptide
LOCATION: 46..87
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.9
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                                                                                                                                                                  NAME/KEY: polyA_signal LOCATION: 1363..1368
                                                                                                                                                                                                                            ; NAME/KEY: polyA_site
; LOCATION: 1382..1394
US-09-247-155-76
LOCATION: 46..675
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                        FEATURE:
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RESULT 8 US-08-887-534A-22

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210 IGGALTIGACAGCCCCATCAGGGCCGGGTIGGTAATATTCTACAATIGGGAAGTAAGCTGA 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 GAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGTTGAATGACTGGCTAACAAAAA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 AAATTICTATGATTCTT--GAAACATTAAAGAATCAATATGAAGCATTAGCTTATAAAAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 1845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 36.6; DB 4; Length 184
48.0%; Pred. No. 0.57;
tive 0; Mismatches 144; Indels
                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
                                                APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450 CAGAAGAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGA 490
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                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA (genomic) (p14c15)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28341/33996
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/887,534A
                                                                                                                                                                                                                            Illinois
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA (genom
                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
Sequence 22, Application US/08887534A Patent No. 6455323 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Rin-Laures, Li-Hsien REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 28:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1845 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 48.09
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS TOCATION: 856..1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-887-534A-22
                                                                                                                                                                                                                                                                      90909
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LOCATION:
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US-09-007-005-17
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                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 CAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTAC 521
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Sequence 17, Application US/09007005B
Patent NO. 625858
GENERAL INFORMATION
APPLICANT: Sostak, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: FUSIONS
FILE OF INVENTION: FUSIONS
FILE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT FILING DATE: 1998-01-14
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE FEASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09244796

Patent No. 6281344

GENERAL INFORMATION:
APPLICANT: SCOSTAR, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: LAUGH W.
TITLE OF INVENTION: FUSIONS
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PASSEQ for Windows Version 4.0

SEQ ID NO 17
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.8%; Score 36.2; DB 4;
Best Local Similarity 6.1%; Pred. No. 0.22;
Matches 14; Conservative 99; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATION: (1)...(289)
CTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
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                                                                                                                                                                                                                                       Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Racie, Lisa A.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                Query Match 1.8%; Score 36.2; DB 4; I Best Local Similarity 6.1%; Pred. No. 0.22; Matches 14; Conservative 99; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/014,969
                                           FEATURE: OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/09014969
Patent No. 5965397
                                                                                                             ; NAME/KEY: misc_feature
; LCCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: MCOSY, John M.
APPLICANT: LaVallie, Edward
TYPE: RNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02140
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US-09-014-969-14
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COUNTRY:
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                                                                                            FEATURE:
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nucleic acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 193, Application US/08630915A
Patent No. 6308820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                      304 TGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGGGTAGCTAG 363
                                                                                                                                                                244 TATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAAAC 303
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                 364 CATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                             424 AGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAA 478
                                                                                                                             ;0
                                                                                       Query Match 1.8%; Score 36.2; DB 2; Length 2447; Best Local Similarity 46.8%; Pred. No. 0.91; Matches 110; Conservative 1; Mismatches 124; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/630,915A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                 ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA '
US-09-014-969-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: ALCCOLLECT: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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US-08-630-915A-193
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Pred. No. 0.57;
0; Mismatches 37; Indels (
1.8%; Score 36; DB 4; Length 2873; 52.7%; Pred. No. 1.2;
                                           70; Indels
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TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 CTGGCTAACAAAACAGAAGAAGAACAAGGAAAA 470
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Sequence 13, Application US/09461474
Patent No. 6278042
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Safalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: BB1303 US NA CURRENT APPLICATION NUMBER: US/09/461,474 CURRENT FILING DATE: 1999-12-14 EARLIER APPLICATION NUMBER: 60/112,562 EARLIER FILING DATE: 1998-12-16 NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
                                                                                                                                                                                                                                                                    533 GIGCTICAAGAAGAICTAGAACAAGAAC 560
                                                                                                                                                                                                                                                                                                          162 ACACAAGAAAAATTCAAGAAGAGGAAC 189
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08139937
Patent No. 5821070
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMPBELL AND FLORES
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Best Local Similarity 61.1%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Office 97
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                                             78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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                         Similarity
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LENGTH: 790
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    Query Match
                           Best Local
                                             Matches
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GENERAL INFORMATION:
APPLICANT: BOARD OF RECENTS OF THE UNIVERSITY OF TEXAS SYSTEM
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.7%; Score 35.6; DB 1; Length 4868; 51.9%; Pred. No. 2.2;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/IIS94/112210
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2041 TGAAAGAAAAATCAAGCACTGCCATGGAGATGCT 2074
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                                                                                        CLASSIFCATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/979,156
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 9370
TELEPHONE: 619-535-9001
TELEPHONE: 619-535-9001
TELEPHONE: 619-535-9001
TELEPHONE: 619-535-9001
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
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19-NOV-1993
                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,937
FILING DATE: 20-OCT-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
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NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: FP-C
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEPAS: 619-535-8949
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                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4868 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Matches 80; Conservative
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     SOFTWARE:
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                                                                                                                                                      Ouery Match 1.7%; Score 35.6; DB 5; Length 4868; Best Local Similarity 51.9%; Pred. No. 2.2;
                                                                                                                                                                                                 74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           564 TCAGGGICAAITCICICACTCACAIGGIGGIGGI 597
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                4868 base pairs
                                                                                                                                                                                                   80; Conservative
SEQUENCE CHARACTERISTICS:
                                                           single
                                      TYPE: nucleic acid
STRANDEDNESS: singl
                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

April 25, 2003, 17:39:49 ; Search time 135.61 Seconds Run on:

(without alignments) 16376.941 Million cell updates/sec

US-09-845-416-12_COPY_960_3000 2041 Perfect score: Title:

1 tccttcacagcatttggaag......ttctgcatgattctatccaa 2041 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Scoring table:

Total number of hits satisfying chosen parameters: 709820 seqs, 544064369 residues

Minimum DB seq length: 0 Maximum DB seq length: 5000

Maximum Match 100% Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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'cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
'cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:* Published_Applications_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.

Sequence 442, App Sequence 442, App Sequence 410, Ap Sequence 212, App Sequence 204, App Sequence 204, App Sequence 21956, A Sequence 6092, Ap Sequence 11083, A Sequence 27715, A Sequence 10742, A Sequence 24084, A Sequence 157, App Sequence 18355, A Sequence 183, App Sequence 183, App Sequence 183, App Sequence 343, App Sequence 183, App Description US-10-184-644-442 US-10-184-634-442 0 US-09-960-352-4010 US-10-123-155-212 US-09-864-761-11083 US-09-864-761-27715 US-09-960-352-10742 US-09-960-253-157 US-09-864-761-18355 US-09-864-761-21956 US-09-864-761-6092 US-09-864-864-204 US-09-960-352-12395 US-09-822-846-343 US-09-918-995-24084 US-10-174-590-183 US-10-176-758-183 US-10-175-737-183 US-10-173-706-183 SUMMARIES 10 10 10 10 Match Length DB 1381 1594 1594 1594 1594 Query Score 177 153.4 151 190.2 Result

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ALIGNMENTS

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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Rank, Wensheng
ITTLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL COURRANT FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-27
PRIOR PAPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/US01/00666
PRIOR PAPLICATION NUMBER: PCT/US01/00669
PRIOR PAPLICATION NUMBER: PCT/US01/00669
PRIOR PAPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
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                                                 Sequence 21956, Application US/09864761
Patent No. US20020048763A1
US-09-864-761-21956
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APPLICATION NUMBER: PCT/US01/00666
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMBN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GNB EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GNB EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GNB EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-26
PRIOR PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-010-04
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-07
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Best Local Similarity 98.5%; Pred. No. 1.1e-47;
Matches 192; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: EXPRESSED IN PLACEBTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BORD MARROW, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BOUT LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN MELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN MELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: WISSPROT HIT: P11532, EVALUE 2.00e-30

OTHER INFORMATION: NT HIT: 915032282, EVALUE 1.00e-103
     PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEC ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEC ID NO 21256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6092, Application US/09864761 Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                IYPE: DNA
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APPLICANT: Penn, Sharron G.
APPLICANT: Bank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO*
FILLE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
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100.0%; Pred. No. 1.8e-43;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PLILNG DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
                           PRIOR PAPLICATION NUMBER: PCT/USO1/00667
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO AC004468.1
OTHER INFORMATION: EXPRESSED IN PLACE
OTHER INFORMATION: EXPRESSED IN LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.7%
Best Local Similarity 100.0
Matches 177; Conservative
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OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88
IS-09-864-761-11083
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                                                                                              PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GE 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                       PRIOR APPLICATION NUMBER: US 60/180,312
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ORGANISM: Homo sapiens
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433 TGAAGACCTAAAACGCCAAGTACAACAACATAAGG 467

☆ á JS-09-864-761-27715

RESULT 4

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Sequence 27715, Application US/09864761

GENERAL INFORMATION:
APPLICANT: Nenn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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100.0%; Pred. No. 7.4e-36;
Live 0; Mismatches 0; Indels
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.08

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.08

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81

OTHER INFORMATION: WITHIT: MI853.1, EVALUE 6.00e-80

OTHER INFORMATION: SWISSPROT HIT: P11532, EVALUE 4.00e-08
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                                                                                                                                                                                                                                                                                                                                 TITLE REFERENCE: AGENE EAFRESSION ANALYSI:
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/20,366
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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2027 CATGA 2031
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US-09-960-253-157
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LENGTH: 2247
LENGTH: 449
                                                                                                                                                                        Query Match
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                                                                                                                                                                                                              Sequence 10742, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10742
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                                 442 AACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGA 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 ITTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGA 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 43; DB 10; Length 436; 48.6%; Pred. No. 0.014; tive 0; Mismatches 125; Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PPLICATICATICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
: ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 46-LIB3058-032-Q1-K1-D10
JS-09-960-352-10742
                                                                                     NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24084, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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Best Local Similarity 48.65
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       258 GTTAAAAGCTATGTTAGCAACCATGTGTGGTGGAAAAATGCTGGACAAATTGAGATATGTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 TTCTCCCAGATGTCAGATTCCAATGGCTTAATGATATTAGCAAGTTTGACCAGTTTCTG 377
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                                                                                                                                                                                                                                                     DB 9; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Benson, Darin R.
APPLICANT: Mohamath, Raodoh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFRENCE: 210121.556
CURRENT APPLICATION NUMBER: US/09/960,253
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                   89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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                                                                                                                                                                                                                                              / Match 2.1%; Score 42.6; DB 9 Local Similarity 51.9%; Pred. No. 0.019; nes 96; Conservative 0; Mismatches E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 157, Application US/09960253 Patent No. US20020123619A1
                                                                                                                   COCATION: (1)...(449)
CTHER INFORMATION: n = A,T,C or US-09-918-995-24084
                                                                                  NAME/KEY: misc_feature
TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-960-253-157
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ORGANISM: Homo Sapien
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GENERAL INFORMATION:
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                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
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N: EXPRESSED IN HELLA, SIGNAL = 2.8
N: EXPRESSED IN HELLA, SIGNAL = 2.8
N: EXPRESSED IN LONG, SIGNAL = 1.4
N: EXPRESSED IN FORTAL LIVER, SIGNAL = 2.6
N: EXPRESSED IN FORTAL, SIGNAL = 1.9
N: EXPRESSED IN MEART, SIGNAL = 1.9
N: EXPRESSED IN PLACENTA, SIGNAL = 1.9
N: EXPRESSED IN PLACENTA, SIGNAL = 1.9
N: EXPRESSED IN ADDLT LIVER, SIGNAL = 1.6
N: EXPRESSED IN BT474, SIGNAL = 2.2
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LENGTH: 423
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Pred. No. 0.024;
0; Mismatches 138;
                                                                                                                                                                                                                                                                                  CONNENT RETLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                       Sequence 18355, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAP TO AC010133.1
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ORGANISM: Homo sapiens
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INFORMATION:
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OTHER INFORMATION:
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US-09-864-761-18355
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APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: APOGLOWIN SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1367 GACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCTG 1426
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                                                     335 TCAAGATGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTT 394
                                                                                                                                                                    395 TTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAA 454
                                                                                                                                                                                                                                                                                GAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAAGACCTAAAACGC 514
                                                                                                                                                                                                                                                                                                                                                                                                    309 R.YS..T.M.RBAKD.BAS.MNR..SDMC.T.W.SBB.CYHMB...HN.S.RMN...BMH 250
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3.7%; Pred. No. 0.033;
Eve 132; Mismatches 214; Indels
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Publication No. US20030044930A1
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Goddard, Audrey
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Best Local Similarity 51.2 Matches 148; Conservative

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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 18-BOVMS1-007-Q1-E1-E5
US-09-960-352-4010
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                                   Sequence 4010, Application US/09960352 Patent No. US20020137139A1
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Wood, William
                                                                                                         GENERAL INFORMATION: APPLICANT: Warren, Wesley C.
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APPLICANT: Beresini, Maureen
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Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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Filvaroff, Ellen
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US-09-960-352-4010/c
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                                       1667 CTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCACACAACCTC 1726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 442, Application US/10184634 Publication No. US20030068684A1
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Gurney, Austin L.
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Best Local Similarity 8.7%; But Local Similarity 8.7%; Bu
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S..H.A.RHBMBCYSB..M 51
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APPLICANT: Baker, Kevin P.
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ORGANISM: Homo Sapien
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US-10-184-634-442

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LENGTH: 440 SEQ ID NO 442

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TILE REFERENCE: P3330R1230 CURRENT APPLICATION NUMBER: US/10/123,155 CURRENT FILING DATE: 2002-04-15
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                                                                                                                                                                                                                                                                                                                                                            84 AAACAGCTTTAGAAGAAGTATTATCGTGCCTTCTTTCTGCTGAGGACACATTGCAAGCAC 143
                                                                                                                                                                                                                                                                                                                                                                                                                       89 AWRPALYLAALDCAEETNSAVCRDFNIPGFPTVRFFKAFTKNGSGAVFPVAGADVQTLRE 148
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                                                                                                                                                                                                                                            Length 747;
                                                                                                                                                                                                                                                                                                 Conservative 172; Mismatches 410; Indels
   - See Palm or File Wrapper
                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                         2.0%; Score 40.6; DE 11.0%; Pred. No. 0.11;
Prior Application removed - NUMBER OF SEQ ID NOS: 550
                                                                                                                                               ORGANISM: Homo Sapien US-10-123-155-212
                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 72; Conserv
                                                       SEQ ID NO 212
LENGTH: 747
                                                                                                                      TYPE: PRT
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; Sequence 204, Application US/09864864
; Patent No. US20020102679A1
                                                                                               APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Dillon, Davin C. APPLICANT: Lodes, Michael J. APPLICANT: Lodes, Michael J. APPLICANT: Fling, Steve P.
                                                                                                                                                                                                                                                                           Mannion, Jane
Benson, Darin R.
                                                                                                                                                                                                                                                                                                                    Carter, Darrick
                                                                                GENERAL INFORMATION:
RESULT 13
US-09-864-864-204
                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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520 ACAACAACATAAGGTGCTT 538

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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 GGATCTCCAGAAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGG 459
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                                                                                                                                                                                                                                                                                                                    Length 428
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 53-LIB3058-009-Q1-K1-F2
US-09-960-352-12395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 GGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 GGACTCAAAAATTTAATGTGTCCAACAGAAGAATCGATGAAG 369
                                                                                                                                                                                                                                                                                                               Score 40.4; DB 10;
Pred. No. 0.086;
0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.0%; Score 39.8; DB 10;
ilarity 47.1%; Pred. No. 0.13;
Conservative 0; Mismatches 137;
                      TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN C CURRENT APPLICATION NUMBER: US/09/864,864 CURRENT FILING DATE: 2001-05-23 NUMBER OF SEQ ID NOS: 341 SOFTWARE: Corixa Invention Disclosure Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12395, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                    2.0%;
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.19
Matches 86; Conservative
                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-864-864-204
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Matches 122; Conserva
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                                                                                                                                                                     SEQ ID NO 204
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173 ATCTAGACACAGAATCCTT 155
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RESULT 15 US-09-822-846-343/c

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APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS FILE REFERENCE: G.M. 6400
CURRENT PILLING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2000-04-06
RIOR FILING DATE: 2000-04-06
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 343
LENGTH: 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.9%; Score 39.6; DB 9; Length 1381; Best Local Similarity 60.0%; Pred. No. 0.34; Matches 66; Conservative 0; Mismatches 44; Indels 0;
Sequence 343, Application US/09822846
Publication No. US20030027139A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Evans, Cheryl
                                                                                                                                                                     Merberg, David
Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Bowman, Michael R.
Spanlding, Vikki
Wong, Gordon G.
Clark, Hilary
                                                                                                                                                                                                                                                                                                                                            Fechtel, Kim
Howes, Steven H.
Resnick, Richard J.
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; ORGANISM: Xenopus sp.
US-09-822-846-343
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APPLICANT:
APPLICANT:
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APPLICANT:
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369 AAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGGT 428

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Search completed: April 25, 2003, 23:58:31 Job time: 145.776 secs

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April 25, 2003, 07:56:07 ; Search time 3411.5 Seconds (without alignments) 17070.103 Million cell updates/sec
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                                                                                                                                                                                                                                                           3813070
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                        US-09-845-416-14_COPY_1000_3000
2001
                                             OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 5000
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Database :

Sequence:

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Run on:

Searched:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

% Query Score Match Length	1332 66.6 4402 6 830220	1269.2 63.4 4402 6 E3021	776.6 38.8 3275 10 MUSDYS MIROTE MIRO	735.4 36.8 4075 6 E30221 R3021 Short.	731.2 36.5 3747 6 E30218 E30218 E30218 Chort.	677.6 33.9 3163 6 E30223 E30223 Short	615.4 30.8 2654 5 FSCDYSTRO M37645 TOTTLE	612.2 30.6 630 9 HSDMDF1 x06179 Human	569. 28.4 2110 9 HUMDMDXX M92650 Human	554 26 4 4658 9 BC028720	528 26 1052 DAF 399031 AF 399031 Dan	528 20:4 1908 9 HSDMDAI X06178 H 518 25:9 1240 10 PARADRY3	506.6 25.3 3161 10 MMCHTPPPH	475 23.7 3073 10 AF195788 AF195700 PARTICELLI	475 23.7 3140 10 AF195787 AF195787 BEFFELUS	470.2 23.5 3499 9 HSU43519 U43519	458.8 22.9 3172 6 E30222	387.6 19.4 1961 5 XLDYSTROP	350.6 17 E 1003 F 250.5	345.8 17 3 2650 3 CDMSTROP X99702 S	334.2 16.7 1898 10 BC024140	265 13.2 506 10 AB011666 AB0111	264.2 13.2 1428 5 SCU43517 143517 SC	263.6 13.2 1482 5 XLUTROPHI x99701	235.4 12.8 1737 5 SCUTROPHI X99703	232.2 11 6 1440 5 CHAPELO	225.2 11.3 1428 10 MMIN 35.00 (43518 Gobius Sp.	213.2 10.7 1413 3 ASDYSTROP	210.8 10.5 1431 3 PSDYSTROP x99738 p	203 10.1 351 9 HUMDYST06 M86889 H. Sapiene	1963 9.8 1338 3 BLDYSTROP X99736 B.lanceola	18 2 3 2 2 5 9 8 2 3 4 1 AF213411 AF213411 Homo sa	186 2 9 3 1500 6 AX10/969 AX107969	180.4 9.0 454 9 AXIO7970	179.8 9 0 374 10 GENERALD AF213415	175.4 8 8 1720 3 CTENERRO	160.2 8 6 645 9 XECTION X99/56 C.intes	157 7.8 300 9 S38776	151 7.5 332 9 HUMDYST01	150.2 7.5 2962 3 DMDYTTRO x903757 n molecus	150 7.5 234 9 86097
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ALIGNMENTS

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DNA			-1999; ENTER O
dq			NOV
4402 bp			3 24-
E30220 Shortened dystrophin. E30220.1 GI:13017027	JP 1999318467-A/3. unidentified. unidentified	unclassified. 1 (bases 1 to 4402) Sinichi,T. Shortened dystrophin	Patent: JP 1999318467-A 3 24-NOV-1999; SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
RESULT 1 E30220 LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL

	E		יום יון		qq	1915	TTTAGTGC?
COMMENT	±	P. V. O.	57-A/3		Qy	780	AAAGATCAA
			08-MAY-1998 JP 199814213	34	qq	1975	AAAGATCAA
		PI PC	SINICHI TAKEDA C12N15/09, A61K48/00, C12N1	N15/00	QY	840	GAAAAGAAA
		ខូខូ	Strandedness: Both; Topology: Linear;		QQ	2002	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
		FH		n/Qualifiers 2	ΟY	006	CTGAAGAA
FEATURE	SES	FT	cation/Qua	/organism='Unidentified'. Lifiers	qq	2002	: : : : : : : : : : : : : : : : : : : :
	source		14402 /organism="unidenti	fied"	Οy	096	TGGGATAA
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ORIGIN	z				Qy	1020	GAACTTCA
Que	Query Match	cch	66.6%; SCO 83.8%; Pre	1332; DB 6; Length 4402; No. 0;	qa	2002	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Mat	ches 1	1677;	Matches 1677; Conservative 0; Miss		QY	1080	GGATCCTG
		GGCAGT	ICATTGATGGAGAGTGAAGTAAAC	GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA 60	qq	2002	
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qq	1315 G	SATGTG	SAAGTGGTGAAAGACCAGTTTCAT	GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGTACATGATGGATTTGACA 1374	Oy	1260	GAAGACCT
٥y	181	SCCCAT	CAGGGCCGGGTTGGTAATTCTA	GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240	QQ	2131	GAAGACCT
qq	1375	GCCCAT	CAGGCCCGGTTGGTAATATTCTA		QY	1320	CTGCATGA
Οÿ		AAATTE	TCAGAAGATGAAGAAACTGAAGTE	AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 300	QO	2191	CTGCATGA
qq		AAATT!	TCAGAAGATGAAGAAACTGAAGT		Óλ	1380	CAGGGTCC
δλ	301	TGGGA	TGCCTCAGGGTAGCTAGCATGGAP	TGGGAATGCCTCAGGGTAGCTAGCATGGAAAACAAAGCAATTTACATAGAGTTTAATG 300	qq	2251	-
qq		TGGGA	TGCCTCAGGGTAGCTAGCATGGAA	} -	Óγ	1440	ACTCAAAC
oy .		GATCT	CAGAATC-GAAACTGAAAGAGTTC	GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAACAGAAGAAAA 419	qa	2311	
qq		GATCT(CAGAATCAGAAACTGAAAGAGTTT		QΫ	1500	CTGAATAA
0y	0	ACAAG(AAAATGGAGGAAGAGCCTCTTGG	ACAAGGAAAATGGAGGAAGACCTCTTGGACCTGATCTTGAGGACCTAAAACCCAAAAA */>	qq	2371	CTGAATA
qq		ACAAG	AAAATGGAGGAAGAGCCTCTTGG		Qy	1560	GCCCTTTC
ΟŊ	0	CAACA	CATAAGGTGCTTCAAGAAGATCT	CAACAACATCATCATCAAGAACTCTAGAACAAGAACAAGTCAGGGTCAATTCTCTC 559	qq	2431	- Ō
qq		CAACA	.CATAAGGTGCTTCAAGAAGATCT.		Óγ	1620	
οy		ACTCA	ATGGTGGTGGTAGTTGATGAATC	ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTTTGGAA 399	QC	2491	-5
qq		ACTCA	ATGGTGGTGGTAGTTGATGAATC		Qy	1680	TATGACC
δλ	00 1	GAACA	CTTAAGGTATTGGGAGATCGATG	GAACAACTTAAGGTATTGGGAGTCGATGGCCAAACATCTGTAGATGGACACACAGACGC 059 	qa	2551	
g G			ACTTANGGIAITGGGAGAICGAIG	7.1	ΟŊ	1740	TGTCTGA
Qy Dp	1855		CCTTTTACAAGACATCCTTCTCAA 	TGGGTTCTTTTACAAGACATCCTCTCAAATGCCAACGCTIACIGAAAAAAAAAA	qq	2611	
ογ	0		GCATGGCTTTCAGAAAAAAAAAAA	TTTAGTGGCTTTCAGAAAAAGAAGATGCAGTGAACAAGATTCACACAAGGTTT 779	Å A	2671	
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AACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTG 1799
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                                                                                                                                                                                                               ATTTAGTCCAAAAACTTGAAAAGAGTACAGCACAGACCCTTGAAAGACTCCAG 1019
                                                                                                                                                                                                                                                                         AAGAGGCCACGGATGAGCTGGACCTGCGCCCAAGCTGAGGTGATCAAG 1079
                                                                                                                                                                                                                                                                                                                                    GGCAGCCCGTGGGCGATCTCCTCTTGACTCTCCCAAGATCACCTCGAGAAA 1139
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                                                                                       NAAAGCAATCCATGGGCAAACTGTATTCACTCAAACAAGATCTTCTTTCAACA 899
                                                                                                                                                  ATAAGTCAGTGACCCAGAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT 959
                              NAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTAAAAAGCGGATCTA 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAATGAAATGTTATCAAGT-----
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Db 1495 TGG Qy 361 GAY Db 1555 GAY QY 420 ACZ QY 480 CAAC QY 480 CAAC	Db 1675 III Qy 540 ACT Qy 600 GAA Qy 600 GAA Db 1795 GAA Qy 660 TGG Db 1830 Qy 720 TTT Db 1830 Qy 780 AAA	Oy 840 GAA Oy 840 GAA Db 1830 Oy 900 CTG Db 1830 Oy 960 TGG	QQ 1020 GAA DD 1891 GAA QY 1080 GGA QY 1080 GGA QY 1140 GTC QY 1200 CTT QY 1200 CTT QY 1260 GAAC QY 1260 GAAC QY 131 GAAC QY 1320 CTGC QY 1111
OY 1860 CTTTCAAGCAAGTGGCAAGTTCAACAGATTTTGTGACCAGGCGGGGCTGGCCTCCTT 1919	RESULT 2 E30219	PR SINICHI TAKEDA PC C12N15/09, A61K48/00, C12N15/00 CC Strandedness: Both; CC Topology: Linear; FH Key Location/Qualifiers FT Source /Organism='Unidentified'. FATURES Location/Qualifiers 14402 /Organism="unidentified" Mb_xref="taxon:32644" ORIGIN PR SINICHI TAKEDA Location/Qualifiers //db_xref="taxon:32644" ORIGIN	Query Match 63.4%; Score 1269_2; DB 6; Length 4402; Best Local Similarity 82.1%; Pred. No. 4.1e-309; 35 Gaps 3; Matches 1644; Conservative 0; Mismatches 33; Indels 325; Gaps 3; QY 1 GGCAGTTCATTGATGAGAGTAACAGCTGGACCGTTATCAACAGCATTTGAACAGAGAA 10 10 111111111111111111111111111111111111

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ATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTICAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAG 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCTGGCAGCCCGTGGGCGATCTCCTTCATTGACTCTCCCAAGATCACCTCGAGAAA 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTG 1259
                                                                                                                      AAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTA 479
                                                                                                                                                                                                                                                             TCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599
                                                                                                                                                                                                                                                                                                                              ACAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG 1319
                                                                                                                                                                                                                                                                                                                                                                                                 GGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAG 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGTGCATGGCTTTCAGAAAAAAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTA 839
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                                                                                                                                                                                         ACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTC
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/translation="gyaftqaayvatsdstqspypsohleaprdksldsslmetevnl
bsyqtaleevlswllsaedtlraqgeisndveevkeofhahegfmmdltshqglvgnv
lQlgsqlvgkgklsedbeaevqeomnllnsrweclrvasmerqsklhkvlmdlongkl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservation of the Duchenne muscular dystrophy gene in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1860 CTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCCTT 1919
                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAATAATGTCAGATTCTCAGGTTATAGGACTGCCATGAAACTCCGAAGAGTGCAGAAG 1559
                                                                                                                                                                                                        1680 TATGACCGCCTGGAGCAAGAGCACAACTTTGGTCAACGTCCCTCTCTGCGTGGATATG 1739
                                                                                                                                                                                                                                                                                                                                                          1740 TGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTG 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATAC 1859
                                                       CTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAG 2430
                                                                                                                                                                                     GCCCTTTGCTTGGATCTTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAAC 1619
                                                                                                                                                                                                                                                              CTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATT 1679
2251 CAGGGTCCCTGGGAGAGACCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAG 2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2671 TCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATAC
                                     1440 ACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monaco, A.P., Feener, C.C. and Kunkel, L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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M18025
M18025.1 GI:192971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 238 (4825), 347-350 (1987)
88018015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA37530.1"
/db_xref="GI:192972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dystrophin. Mouse adult heart, cDNA to mRNA. Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3275 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2851 AACATTGAGCCAAGTGTCCGGA 2872
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Hoffman, E.P., Monaco,
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QTLTDGGVMDELINEELETFNSRWRELHEEAVRKQKLLEQSIQSAQEIEKSLHLIQES
LEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDIOTIOPSLNSVNEGGOKIKSEAELEFASRLETELRELNTOWDHICROVYTRKEALK
AGLDKTVSLOKDLSEMHEWMTQAEEEYLERDFEYKTPDELQTAVEEMKRAKEEALOKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
KELHDWLTKTEERTKKMEEEPFGPDLEDLKCQVQQHKVLQEDLEQEQVRVNSLTHMVV
                                            VVDESSGDHATAALEEQLKVLGDRWANICRWTEDRWIVLQDILLKWQHFTEEQCLFST
                                                                                        WISEKEDAMKNIQTSGFKDQNEMMSSLHKISTLKIDLEKKKPTMEKLSSLNQDLLSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKVKLLTETVNSVIAHAPPSAQEALKKELETLTTNYQWLCTRLNGKCKTLEEVWACWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAAGGTCAATTCTCTC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 ACTCACATGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600 GAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAAGGAAAATGGAGGAAGGACCTCTTGGACCTGATCTTGAAGACCTAAAAACGCCAAGTA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642 ACTCACATGGTAGTAGTGGTTGATGAATCCAGCGGTGATCATGCAACAGCTGCTTTGGAA 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GIAITATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTCTAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGATTTGACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 TCTCATCAAGGACTTGTTGGTAATGTTCTACAGTTAGGAAGTCAACTAGTTGGAAAAGGG 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      758 t
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PAT 18-JUN-2001
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SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
OS Unidentified
                                                                                                           780 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTA 839
                                                                                          840 GAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAACAAGATCTTCTTTCAACA 899
                                                     1257 CTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGG 1316
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Gaps
                                                                                                                                              900 CTGAAGAATAAGTCAGTGACCCAGAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGT
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                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                 960 TGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCACAGA 1002
                                                                                                                                                                                                               1062 IGGGACAATTTAACCCAAAAACTTGAAAAGAGTTCAGCACAAA 1104
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Strandedness: Both;
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                                                                                                                                                                                                                                                                                                 4075 bp
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910 c 936 g
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08-MAY-1998 JP 1998142134
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JP 1999318467-A/4.
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                                                                                                                                                                                                                                                                                                                                                                 unidentified.
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ACCESSION
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PAT 18-JUN-2001
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SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
1497 GACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAG 1556
              2041 GACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAG 2100
                                                 AAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCAC 1616
                                                             1617 AACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACT 1676
                                                                                                                                                                                                ATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTC 1796
                                                                                                                                                                                                                                                             TACCTITICAAGCAAGTGGCAAGTTCAACAGGATTTTTGTGACCAGCGAGGCTGGGCCTC 1916
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Strandedness: Both;

    .3747
    /organism="unidentified"

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JP 1999318467-A/1
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E30218
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PAT 18-JUN-2001
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SCIENCE & TECH AGENCY, NATIONAL CENTER OF NEUROLOGY AND PSYCHIATRY
PN JP 1999318467-A/A
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                                                                                        TCCAGGGTCCCTGGGAGAGACCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACG 1437
                                TGGAAGACCTGAACCACAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGC 1317
                                           Gaps
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Pred. No. 2.1e-173;
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            0; Mismatches
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Sinichi,T.
Shortened dystrophin
98.98;
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             Conservative
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 Best Local Similarity
Matches 736; Conserv
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ACCESSION
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                                                                                                                                                                                                  33.9%; Score 677.6; DB 6; Length 3163; 98.7%; Pred. No. 7.1e-160; tive 0; Mismatches 9; Indels 0;
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                                                                                                     organism='Unidentified'
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                                                                               Location/Qualifiers
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                               SINICHI TAKEDA
C12N15/09,A61K48/00,C12N15/00
Strandedness: Both;
                                                                                                                            1. 3163
/organism="unidentified"
/db_xref="taxon:32644"
a 731 c 720 g 78:
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        08-MAY-1998 JP 1998142134
                                                                                                                   Location/Qualifiers
                                                                      Topology: Linear;
                                                                                                                                                                                                                              Matches 683; Conservative
                                                                                                                                                                                                                    Local Similarity
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Query Match
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Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
1 (bases 1 to 2654)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="SGEQWKRLQISLODFLTWMNLKNDELRRQMPIGGDAPTVCQQND VHRIFKRELKAKEPVWSALDTVHLFLADPAIRAPESLLTGPREKIPEENIONVAKRIRYAAEEVKVEWDKLSNRSVDWQKRIDEALKRLLELQDSMDELNLKLRQAEAIKDTWQPVGDLLIDSLQDHIEKVKVFRAEIAPWKENVTHMNDLASGFTPPDIQLSPYNLNQLEDL
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QTTCWDHPKMTELYQSLADLNNVRFSAYRTAMKLRRLQKALCLDLLSLPSACEAFDQH
NLKQWDQLLDLILEINCLTSIYDRLEQGHSNLVNWPLCYDWCLNWLLNVDTGRTGKI
NEVNDQLLDLILEINCLTSIYDRLEQGHSNLVNWPLCYDMCLNWLLNVDTGRTGKI
SYLSFKSGIMSMCKAHLEDRYRYLFKQTGFCDQRRLGLLLHEAINIPRQLEVA
SFGGSNIEPSVRSCFQFANNKPEIERALFLDWWRLEPQSLVWMPVLHRVAAAFTAKHQ
AKCNICKECPIIGFRYRSLKHFNYDVCQSCFFSGRTAKGHKMHYPMVEYCTPTTSGED
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PEMMPISPQSPRDAELIAEAKLLRQHKGRLEARMQILEDHNKQLESQLHRLRQLLEQP
QAEVRVNGTSVSSPSTSSQRSDSSQPVLLHGVGSQTSGILGEDDLLSAPQSTSSELED
VMEQLSSSFPSSQRRDTPGKKMKEVPM"
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QLSHDDTHSRIEHYLSRLAEMENRNGSYLNDSISPNESIDDEHLLIQHYCQSLNQESP
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                                                                                                                                                                                                                                                                                         2 (bases 1 to 2654)
Ravin,A.J., Dyer,S.M., Yeadon,J.E. and Burden,S.J.
Multiple dystrophin isoforms are associated with the postsynaptic membrane of Torpedo electric organ
J. Physiol. (Paris) 85 (3), 131-133 (1991)
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                                                                                                                                                                                          Yeadon, J.E., Lin, H., Dyer, S.M. and Burden, S.J. Dystrophin is a component of the subsynaptic membrane J. Cell Biol. 115 (4), 1069-1076 (1991)
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Torpedo californica dystrophin mRNA, 3' end.
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                                                                          Torpedo californica, cDNA to mRNA.
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/db_xref="G1:397971"
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M37645.1 GI:397970
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Matches 766;
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linear PRI 28-MAR-1991
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                      1165 CGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGG 1224
                                                                                                                              1225 GCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGC 1284
                                                                                                                                                                                                      1285 ITCIGCAGGIGGCCGTCGAGGACCGAGTCAGGCAGCIGCATGAAGCCCCACAGGGACTITG 1344
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613 ATAICCAATIATCCCCGTACAATCTAAACCAGTTGGAGGATCTGAACACACGGTGGAAAC
                                                                                                                                                                                                                                                                                                                                                                              1585 TGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGACCAGCCCATGG
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X06179.1 GI:
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REFERENCE

1105 TCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTG 1164

ð Dp δ g 602 GCCGTTTTAAAAGCGGATCTAAAAAAAA 630

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819 GCCGTTTTAAAAGCGGATCTAGAAAAAA

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LTEEQCLFSAWLSEKEDAVNKIHTTGFKDONEMLSSLQKLAVLKADLKK"
Cross, G.S., Speer, A., Rosenthal, A., Forrest, S.M., Smith, T.J., Edwards, Y., Flint, T., Hill, D. and Davies, K.E. Deletions of fetal and adult muscle cDNA in Duchenne and Becker muscular dystrophy patients
EMBO J. 6 (11), 3277-3283 (1987)
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                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Cf16."
/dev_stage="fetus"
1. 630
                                                                                                                                                                                                                                                                                                                     /protein_id="CAA29545.1"
/db_xref="GI:30840"
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Best Local Similarity 99.43
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LEPOSNYWLPVIHRVAAATTAKHOAKCNICKECPIIGFFYRSLKHFNYDIQQSCFFSG
RVAKGHKMHYPWLEYCTPTTSGEDVRDFAKVLKNKFRTKRYFAKHPRMGYLPVQTVLE
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HYCOSINODSPHLQPRSPAQILISLESEERGELERILADLEEENRNLQAEYDRLKQQH
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LHRLRQLLEQQPQAEAKVNGTTVSSPSTSLQRSDSSQPMLLRVVGSQTSDSNGEEDLLS
PPODTSTGLEEVMBQLNNSFPSSRGHNVGSLFHMADDLGRAMESLVSVWTDEEGAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2110)
Lederfein,D., Levy,Z., Augier,N., Mornet,D., Morris,G., Fuchs,O., Yaffe,D. and Nudel,U.
A 71-kilodalton protein is a major product of the Duchenne muscular dystrophy gene in brain and other nonmuscle tissues
Proc. Natl. Acad. Sci. U.S.A. 89 (12), 5346-5350 (1992)
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                            PRI 07-NOV-1994
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M92650
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                                                                                                                                                                                                                                                                                                                                                                              /map="xp21.3" p21.1"
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                                                                                                 Duchenne muscular dystrophy protein.
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                                                                                                                   Homo sapiens brain cDNA to mRNA
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511 c 492 g
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/gene="DMD"
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/gene="DMD"
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RESULT 9
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/db_xref="G1:20379676"

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CDQRRLCLLLLHDSY OI PRQLGEVASFGGSNIEPSVRSCROFANKRPEIEAALFLDWRR

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RVAKGHKMHYPWEYCTPTTSGEDVRDFAKVLKNKFRYRFRYFRYSLGENTSCFFSG

GDMETPYTLINWPVDSAPASSPQLSHDSTRSTEHYASRLAEMENSNGSYLNDSIS

PNESIDDEHLLIOHYCGSLUDSPPEMMPTSRQSPRDAELIAEBERRIADLEEENR

NLQAEVDRLKQQHEHKGLSPLSPPEMMPTSRQSPRDAELIAEBERRIADLEEENR

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VSCVVMMADDEN.S.
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Becker types)"
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                                                                                                                                     /note="Vector: pBluescript"
                                                          /tissue_type="Testis"
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4658 bp mRNA linear PRI 01-MAY-2002
Homo sapiens, dystrophin (muscular dystrophy, Duchenne and Becker
LYPRE), clone MGC:33083 IMAGE:4822807, mRNA, complete cds.
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Contact: MGC help desk
Email: cgapbs=r@mail.nih.gov
Email: cgapbs=r@mail.nih.gov
Email: cgapbs=r@mail.nih.gov
Email: cgapbs=r@mail.nih.gov
Email: dgapbs=r@mail.nih.gov
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Pieror Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
http://www.systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                    1613 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1672
                                                                                                                                                           1673 CACTATITATGACCGCCTGGAGCAAGAGCACAACTITGGTCAACGTCCCTCTCTGCGT 1732
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DEFINITION

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FEATURES

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100.0%; Pred. No. 1.8e-132;
tive 0; Mismatches 0;
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LHRVAAAETAKHQAKCNICKECPIIGFRYRSIKHFNYDICQSCFFSGRVAÄGHKMQYP
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SSPSTASPRSDTSLASLRNAASQTTETMGDDELSSPTQDASTGLEDVIEQLNNSFPHS
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DAIOIPRQLGEVASFGGSNIEPSVRSCFQFANNKFELEASVFLDWMRLEPOSMVMLPV
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                                                                                                                                                                                                                                                                                                                  Dystrophin and Dp71, two products of the DMD gene, show a different
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chases 1 to 3521)
Bolamons-Jimenez,F., Rendon,A. and Strahle,U.
Bolamos-Jimenez,F., Rendon,A. and Strahle,U.
Bulamostionnesign
Submitted (22-JAN-2001) Laboratoire de Physiopathologie Retinienne,
EMI 99-18 INSERM-Universite Louis Pasteur, 1, Place de l'Hopital,
Strasbourg 67091, France
Location/Qualifiers
VRT 20-APR-2001
                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (bases 1 to 3521)

Bolanos-Jimenez, F., Bordais, A., Behra, M., Strahle, U., Sahel, J. and
                                                                                                                                                                                                                                                                                                                                          pattern of expression during embryonic development in zebrafish Mech. Dev. 102 (1-2), 239-241 (2001)
AF339031 3521 bp mRNA linear VRT 20-APP
Danio rerio dystrophin (dmd) mRNA, partial cds, alternatively
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/db_xref="G1:13699250"
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Gaps

3;

26.7%; Score 534; DB 5; Length 3521; 71.4%; Pred. No. 1.2e-123; Aative 0; Mismatches 285; Indels

Conservative

Query Match Best Local Sim Matches 718;

Similarity

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PRI 28-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                             1356 CAGCACTITCTITCCACGICTGTCCAGGGTCCCTGGGAGAGAGCCAICTCGCCAAACAAA 1415
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                                                                            1176 GAGAACGIGAGCCACGICAAIGACCIIGCICGCCAGCIIACCACIIIGGGCAIICAGCIC 1235
                                                                                                                                                                    1301 GATAACGTAAATCATGTTAACCAGCTGGCCTCCACATTTAGACCGTCTGACATTCAGCTT 1360
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                                                                                                                                                                                                                              1296 GCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCCAGCATCT 1355
                                                                                                                                                                                                                                                                                                                       1421 TCCATTGAGGAGCATCTGAGTCAGCTGACCACCTTTAAGGACTTGGG---ACCCTCT 1477
                                                                                                                                                                                                                                                                                                                                                                                   1478 CAGAATTTCCTTCATGCGTCTGTTGAAAGCCCTCTCGAACGCTCTATTTCACCCAACAAT 1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1958 CACCTIGAAGATAAGTACAGATTTTTATTTCGAGAGGTGGCCAGTGCCACAGGCTTCTGT
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X06178.1 GI:30836
Duchenne muscular dystrophy
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EFOLKVLGDRWANICRWTEDRWVLLQDILLKWQRLTEECCLFSAMLSEKEDAVNTHT
TGFKDQNEWLSSLCKLAVLKADLEKKKQSMGKLYSIKQDLLSTLKNKSVTQKTEAWLD
NFARCWDNLVQKLEKSTAQMISQAVTTPQESLTQTTVWETRYTYTREQILVKHAQDE
LPPPPPQKKRQITVDSEIRKRLDVDITTELHSWITTNSEAVLQSEPAIFREGNESDLK
EKVNAIEREKAEKFRKLQDASRSGQALVEQWVNEGVNADSIKQASEQLNSFWIEFCQL
LSEKNWLEYGVNNITAFYNOLQOLEGWTTTAENWLK LQPTTPSEPTAIKSQLKICKDF
VNRLSGLOPQIERLKIQSIALKEKGGPPMFLDADFVPTVHFREQVFSDVAREKELQT
IFDTLPPWRYQEFWRANITRWVQSSFTKLSIPOLSVTDYEIMEGVFSDVAREKELQT
FEDTLEPPREX YGETWASATRTWVQSSFTKLSIPOLSVTDYEIMEGVFSDVAREKELQT
KRYQHIQTKKWAAEVDVFFKEREWPALSIPOLSVTDYEIMEGVESDCQCCC
OSGLYYLSTTVKEWARKAPSEISKYYOSEFEEIEGRWKKLSSQLVCKLEGSDNNKL
KRYGHTQCHARANITAENDALGOLEGATLKKQLKOCKLLVSDIQTIQPSLNSV
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                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                 (bases 1 to 1966)
Cross, G.S., Speer, A., Rosenthal, A., Forrest, S.M., Smith, T.J.,
Edwards, Y., Filit, T., Hill, D. and Davies, K.E.
Deletions of fetal and adult muscle cDNA in Duchenne and Becker
EMBO J. 6 (11), 3277-3283 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 GCCAAGTACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCA 531
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                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA29544.1"
/db_xref="GI:30837"
                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                        /tissue_type="muscle"
/dev_stage="adult"
1. .1966
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99.1%;
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ROD 11-AUG-1993
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RRLQKALCLDLISLSAACDALDQHNLKQNDQPMDILQIIYCLTTIYDRLEGEHNNLVN
VPLCVUVCLNWLLNVYDTGRTGRIRVLSFKTGIISLCKAHLEDKYRYLFKQVASSTGF
CDQRRLGLLLHDSIQIPRQLGEVASFGGSNIEPSVRSGFQFANNKPEIEAALFLDWMR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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892 ITTCAACACTGAAGAATAAGTCAGTGACCCAGAAGACGGAAGCATGGCTGGATAACTTTG 951
                           Group,
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Radcliffe Hospital,
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                                                                                                                                25.9%; Score 518; DB 10; Length 1240; 90.9%; Pred. No. 1.3e-119;
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Apo-dystrophin-3: a 2.2kb transcript from the letter dystrophin glycoprotein binding site
Hum. Mol. Genet. 2 (5), 521-524 (1993)
                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                        R.norvegicus mRNA for APO-dystrophin-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tinsley, J.M.
Direct Submission
Submitted (14-DEC-1992) J.M. Tinsley,
Institute of Molecular Medicine, John
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/cell_line="Schwannowa cells"
/dev_stage="neonatal"
106. 1128
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/protein_id="CAA49423.1"
/db_xref="GI:57914"
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ROD 23-AUG-1995
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Blake, D.J., Schoffeld, J.N., Zuellig, R.A., Gorecki, D.C., Phelps, S.R., Barnard, E.A., Edwards, Y.H. and Davies, K.E. G-utrophin, the autosomal homologue of dystrophin Dpl16, is expressed in sensory ganglia and brain pproc. Natl. Acad. Sci. U.S.A. 92 (9), 3697-3701 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1936 AAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATTGAGCCAAGTG 1995
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TCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAAAATGACC 1635
                                                                           1636 AGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGCCTGGAGC 1695
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                                                                                                 linear
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/clone_lib="adult mouse brain"
/dev_stage="adult"
1. .197
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/function="Unknown"
/standard_name="G-utrophin"
/citation=[1]
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="AU#3"
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X83506
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Blake, D.J.
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                               Length 3161;
       /product="G-utrophin (predicted protein)"
/protein_id="CAA58496.1"
/db_xref="GI:793852"
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                                                                                                                                                                                                                                                                                                                                                                  25.3%; Score 506.6; DB 10; 68.6%; Pred. No. 9.8e-117;
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                                                                 /db_xref="SPTREMBL:Q61636"
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/evidence=experimental
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ROD 02-MAY-2001
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Submitted (18-OCT-1999) Division of Medical and Molecular Genetics,
GKT Medical School, 8th Floor, Guy's Hospital, Guy's Tower, London
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
...___i*. Fortheria: Rodentia; Sciurognathi; Muridae; Murinae;
1885 CAGGATITIGIGACCAGCGCAGGCTGGCCTCCTTCTGCATGATICTATCCAAATTCCAA 1944
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                                                                                                                                                                                                                                     1765 ATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTTTTAAAACTGGCATCATTTCCC 1824
                                                                                                                                                                                                                                                                                                                        /note="splice acceptor AG dinucleotide used by A-form"
200. .3073
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/product="dystrophin-related protein 2 B-form splice
variant"
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Roberts, R.G. and Sheng, M.
Association of dystrophin-related protein 2 (DRP2) with postsynaptic densities in rat brain

Moli. Cell. Neurosci. 16 (5), 674-685 (2000)
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/db_xref="G1:11066167"
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/db_xref="taxon:10116"
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Roberts, R.G. and Sheng, M.
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69. .70
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SVESSAGAFLSQHERELESENSESKOTSPROATUNGELVALLAFREEDENSOFTING
SVESSAGAFLSQHERELESTREEDENSOFTINGELVALLAFREEDINSOFTING
SVESSAGAFLSQHERELESTGAMEELSSTLTQABGVRATWEDIGDLFIDSLPEHIQAIK
LFKEEFSPROEDVKUVKUNDLAHQLAISDVHLSMRSRAFLEDINVRWGQHVVARELKG
LQDAHRDFGPGSQHFLSTSOVDWRERI ISPRKVPYXINHQAQTTCWDHPKMTELYQTL
ADLINITKFSAYRTAMKLRRVQKALRLDLVTLTTALEIFNBHDLQASBHVMDVVEVIHC
LTALVRREEBERGILVNVPLCVDMSLNWLLNVFDSGRSGKMRALSFRTGIACLCGTEV
KEKLQYLFSQVANSGSKCDGRLLHEALLHEATUVRDGVRGCGRSGKRRAGFSFRF
STGRPVTEASQFLEWWNLEPOSSWWLAVLHRYVTVAEQVRHQTRCSITCRQCPTRGFRYR
SLKQFNVDICQTCFLTGRASKGNKLHYPIMEYYTPTSSENMRDFATTLKNKFRSKQY
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FSKHPQRGYLPWQSYLESDCSSTPASSPMLHATTSSENMRDFATTLKNKFRSKQY
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FSKHPQRGYLPWQSYLESDCSSTPASSPMLHATTSSTRIBFASKTABMESGWCSFFN
DSLSPDDSIDEDQYLLRHSSPITDREPAFGGQAPCSMATESKGELEKILAHLEDENNI
LQGELRRLKWQHEBAVEAPTLABGSSREATPDHRNEELLARARILRQHKSRLEFRMQIL
LQGELRRLKWQHEBAVEAPTLESDGNGSAGSSLASSPROSEGSHPREKGGTTPDTE
/translation="MQPLVMQGCPYTLPRCHEWHAADREHHSSSLRNTCPQPQVRAAV
TIPAPPWDGAGDPCLSPKLLNGSVGAVGPLEPSAMNLCWNEIKKKSHNLRARLEAFSD
HSGKLQLPLQEIIDWLSQKDEELSAQLPLQGDVALVQQEKETHAAFWEEVKSKGPYIY
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Best Local Similarity 67.1%; Pred. No. 9.1e-109;
Matches 673; Conservative 0; Mismatches 330;
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Search completed: April 25, 2003, 14:29:27 Job time : 3446.67 secs

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16150.348 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

	Description	Human dystrophin m Adeno-associated v Human dystrophin m Adeno-associated v A rod shortened dy A rod shortened dy Human dystrophin m Adeno-associated v
SUMMARIES	ID	AAD37242 AAD37260 AAD37259 AAZ48568 AAZ48567 AAD37237 AAD37257 AAD37257
	DB	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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аФ	Query Match	100.0 99.5 79.6 79.6 63.4 63.1 63.1
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ALIGNMENTS

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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                    New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain,
                                                                            Human dystrophin minigene delta3447.
         AAD37242 standard; DNA; 3446 BP.
                                                                                                                            Becker muscular dystrophy; ds.
                                                                                                                                                                                                                    27-APR-2001; 2001WO-US13677.
                                                                                                                                                                                                                                           28-APR-2000; 2000US-200777P.
                                                      21-AUG-2002 (first entry)
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                                                                                                                                                                      WO200183695-A2.
                                                                                                                                                                                                                                                                  (XIAO/) XIAO X.
                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                               08-NOV-2001.
                                AAD37242;
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AAD37242
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a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adence-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy in minigene delta347 containing nucleotides 1-1992 (N-terminus, hinge H1 and rods R1, R2 and R3), 8749-10227 (rod R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                           present invention relates to an isolated nucleotide sequence encoding
rod repeats, H1 and H4 domains and a cysteine rich domain of
                                                                               Example 1; Page 53-54; 71pp; English.
                                      dystrophin gene
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Sequence 3446 BP; 1074 A; 766 C; 787 G; 819 T; 0 other;

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	Ga		AGAA			BACA			AGGA			AATG	AATG	AGAA	AGAA	GTAC	GTAC	CTCA	CICA	GAAG	GAAG	CGCT	CGCT	CTTT	CIT
3446	0	TAGAA	TAGA	TITCI	TTTC	ATTT	ATTT	GAAC	GAAC	VATTC	ATTC	TTTT	TTTT	AAGAA	AAGAA	SCCAA	SCCAA	ATTCT	ATTCI	CTTTG	CTTTG	AAGAC	AAGAC	AGTGC	AGTGC
enath	ndels	GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA	AGCTT	GIATIAICGIGGCITCITITCIGCIGAGGACACAIIGCAAGCACAAGGAGAGAIITCIAAI	AGAGA	GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA	GATGG	GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA	GATTG	AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA	CCTA	TGGGAATGCCTCAGGGTAGCTAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATG	ATAGAC	GATCTCCAGAATCGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAA	AACAG	CAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATGTAGAAGACCTAAAACGCCAAGTAC	AAAAC	AACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTCA	GGTCA	CTCACATGGTGGTGGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAG	TGCTG	GACAG		GGGTTCTTTACAAGACATCCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTTT	AGAAC
4:	. E	SAAAC	CANAC	CAAGG	CAAGG	TACAT	TACAT	AAGCT	AAGCI	AATCI	AATC	TTAC	TTAC	CAAA	CAAA	ACCT	ACCT	TCAG	TCAG	CAAC	CAAC	AGATG	AGATG	ACTGA	ACTGA
DB 24	0	TTAT	TIAT	AGCAC	AGCA	9888	.5555v	AAGT	AAGT	GATG	GATG	SCAAT	SCAAT	SCTAA	SCTAA	TGAAG	rgaag	ACAAG	ACAAG	TCACG	TCACG	CTGTA	CTGT2	TCTT	TCTT
. 1.0	0; ches	SACCG	SACCG	TTGCA	TTGCA	CATG	CATG	TTGGG	TIGGG	GAGC	GAGC	CAAAC	CAAAC	ACTG	ACTG	ATCT	ATCT	AAGA	AAGA	SGAGA	SGAGA	AACAT	AACAT	CAACG	CAACG
200	red. No. 0; Mismatches	CCTG	CCTG	CACA	CACA	ATACT	ATACT	FACAA	FACAA	FACAA	TACAA	AAAAA	AAAAA	GAATG	GAATC	ACCTG	ACCTG	AGAAC	AGAAC	TAGT	TAGT	GGCA	GGCA	ATGG	ATGG
, ,	ξΞ.,	GTAAP	GTAA	GAGG	GAGG	TTTC	TTTC/	ATTC	ATTC	GAAG	GAAG	ATGG	ATGG	AGTT	SAGTT	TTGG	TTGG	SATCT	SATCT	SAATC	SAATC	CGATG	CGATG	CTCAP	CTCAP
. 44	. 0	TGAA	TGAA	TGCT	TGCT	ACCAG	ACCAG	STAAT	STAAT	AAACT	AAACT	CTAGC	CTAGG	GAAAG	GAAAG	CCCTC	GCCTC	AGAAC	AGAA	TGAT	TGAT	AGAT	AGAT(CCTT	CCTT
100	100 tive	GAGAG	GAGAG	CTTTC	CTTI	AAAG	AAAG	GTTG	GTTG	GAAG	GAAG	SGTAG	SGTAG	AAACT	AAACT	SAAGA	SAAGA	CTTCA	CITCA	GTAGT	GTAGI	TTGGG	TTGGG	GACAT	GACAT
	ty erva	GATG	GATG	GCTT	SGCTT	regre	rggrg	99005		AAGAT	AAGAT	TCAGG	TCAG	ATCG2	ATCG/	GGAGG	GGAG	GGTG	 GGTG(GGTG	GGTG	GGTA	GGTA	ACAA	ACAA
i ?	imilari ; Cons	TCAT	TCAT	TCGT	TCGT	GAAG	GAAG	CAGG	CAGG	TCAG	ATCAG	ATGCC	ATGCC	CAGA	CCAGA	AAAAT	AAAAT	CATAA	CATAR	ATGGT	ATGGT	CTTAZ	CTTA	CTTT	CTTT
, 4	al Sim 2001;	GCAGT	GCAGT	TATTA	TATTA	ATGTG	ATGTG	CCCAI	CCCA	AATT	AATT	GGGA	GGGA	ATCT	ATCT(AAGG	AAGG	ACAA	AACAA	TCAC	CTCAC	AACAA	AACAA	SGGTT	GGGTT
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721 TINGTGCAIGGCITICAGAAAAAAAGAAGAIGCAGIGAACAAGAITCACACAACIGGCITIA 780
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                                                                                                                                                                                                                                                                                    1021 AACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCTGAGGTGATCAAGG
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                                                                  781 AAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAG
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                       2860 TITICAAGCAAGTGGCAAGTICAACAGGATTITGIGACCAGGGAGGCTGGGGCCTCCTIC 2919
                                                    1861 TTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGCGAGGCTGGGCCTCCTTC 1920
                                                                                                                           1921 IGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCCAGTA 1980
                                                                                                                                               2920 TGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCCAGTA 2979
2800 CITITAAAACIGGGATCATITCCCIGIGIAAAAGCACATITGGAAGACAAGIACAGAIACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4414 BP; 1255 A; 1075 C; 1086 G; 998 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Adeno-associated virus vector plasmid, AAV-MCK-3447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 65-66; 71pp; English.
                                                                                                                                                                                                                            2980 ACATTGAGCCAAGTGTCCGGA 3000
                                                                                                                                                                                                     1981 ACATTGAGCCAAGTGTCCGGA 2001
                                                                                                                                                                                                                                                                                                                                 AAD37260 standard; DNA; 4414
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1937 GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 1996
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                                                                                                                                 GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA 180
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                                              1140 GTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAAGGTGAGCCACGTCAATGAC 1199
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                                                                                                                                                                                                                                                                                                       CAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAGTGCCCTACTATATCAACCACGAG 1439
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2837 GGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTGGAGAAA
                                                                                                                                        CTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTG
                                                                                                                                                                                                                                                                                                                        GTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAAGAACGTGAGCCACGTCAATGAC
                                                                                                            CTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTG
                                                                                                                                                                           GAAGACCTGAACACCCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG
                                                                                                                                                                                                           GAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG
                                                                                                                                                                                                                                           Human dystrophin minigene delta3510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The domerins and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophy in minigene delta3510 containing nucleotides 1-1668 (N-terminus, hinge H1 and rods R1 and R2), 8407-10227 (rods R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to an isolated nucleotide sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                               New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
          Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 79.6%; Score 1593; DB 24; Length 3510; Local Similarity 87.7%; Pred. No. 0; Los 1811; Conservative 0; Mismatches 190; Indels 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3510 BP; 1073 A; 787 C; 828 G; 822 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 51-52; 71pp; English.
                               adeno-associated virus; AAV; Du Becker muscular dystrophy; ds.
                                                                                                                                                                                                                  27-APR-2001; 2001WO-US13677
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361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGA 419

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2079
1420 ACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTA 1479
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                                                                                                                                                                                                                                                                                                         TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTT 719
                                               420 ACAAGGAAAATGGAGGAAGGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTA
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                                                                                                              480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTC
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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
2440 GTCCAGGGTCCCTGGGAGAGACCATCTCGCCAAACAAAGTGCCCTACTATATCAACCAC 2499
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                                                                                                                                                                                                                                     ATTTATGACCGCTGGAGCAGAAGCACAATTTGGTCAACGTCCCTCTGCGTGGAT
                                                                                                                                                                                                                                                                                                       1437 GAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCT
                                        2500 GAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGATCTACCAGTCTTTAGCT
                                                                              GACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAG
                                                                                                                                AAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCAC
                                                                                                                                             AACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACT
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                                                                                                                                                                                                                                                                                          ATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTC
                                                                                                                                                                                                                                                                                                                                              CTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGA
                                                                                                                                                                                                                                                                                                                                                                                                 TACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCAGGCTGGGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                       2920 TACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGCGAGGCTGGGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
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WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -

Example 1; Page 63-65; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammanian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.

Sequence 4476 BP; 1252 A; 1096 C; 1127 G; 1001 T; 0 other;

64; Gaps DB 24; Length 4476; Indels 0; Mismatches 190; r Match 79.6%; Score 1593; Local Similarity 87.7%; Pred. No. 0; Conservative Matches 1811; Query Match

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GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGA

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TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTT 719 = = = = --099

1377 GTCCAGGGTCCCTGGGAGAGGCATCTCGCCAAACAAAGTGCCCTACTATATCAACCAC 1436 3255 1437 GAGACTCAAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCT 1496 1677 ATTIAIGACCGCCTGGAGCAGAGCACAATTTGGTCAACGTCCCTCTCTGCGTGGAT 1736 3496 ATTTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGAT 3555 2596 ACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAG 2655 2656 CCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGAGA 2715 --AAGAGTACAGCACAGACCCTTGAAAGACTC 1016 2896 AAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCCAAGATCACCTCGAG 2955 1137 AAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAGAACGTGAGCCACGTCAAT 1196 2416 TGGGTTCTTTTACAAGACAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAA 2475 2536 GACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAA 2595 2716 GCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAA 2775 886 ATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAGACGCAAGCATGGCTGGA-- 943 720 TITAGIGCATGGCTTTCAGAAAAAGAAGATGCAGIGAACAAGATTCACAACAACTGGCTTT 779 780 AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTAAAAAGCGGATCTA 839 2956 AAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAGA 1497 GACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAG 2776 AAATTGAACCTGCACTCCCCTGACTGGCAGAAAAATAGATGAGACCCTTGAAAGACTC 1017 CAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATC 1077 AAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAG 1197 GACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACT 1257 CTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGG 3136 CAGCIGCAIGAAGCCCACAGGGACITIGGICCAGCAICICAGCACTITCITICCACGICI 3196 GTCCAGGGTCCCTGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCAC 3316 GACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAG 1557 AAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCAC 1617 AACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACT 840 GAAAAGAAAAGCAATCCATGGGCAAACTGTA-979 AACTTGAA--qq q q δλ QQ qq qq g q ŏ pp δ g qq δŏ ŏ q a g g δ q δŽ qq ŏ δλ ŏ QY δŏ Qγ ò Ω

1195 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA 1254

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having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low
                                                                                                                                                                                                       CTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTCAAGTTGCATCCTTTGGGGGC 1976
                                                                                                                                    TACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTC 1916
ATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTC 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A rod shortened dystrophin (deltaDysAH3) encoding nucleotide sequence.
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                3556 AIGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTC
                                                                  CTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGA
                                                                                     Muscular dystrophy; rod domain; adeno-associated virus; AAV;
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P-PSDB; AAY59239
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                               1255 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGTTTCTAAT 1314
                                                                                1315 GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA 1374
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GTATTATCGTGGCTTCTTCTGCTGAGGACACATGCAAGCACAAGGAGAGTTTCTAAT
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Conservative

Similarity

Best Local Sim: Matches 1677;

Query Match

66.6%; Score 1332; DB 21; Length 4402; 83.8%; Pred. No. 0;

1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA 60

immune reaction. The present sequence represents a rod shortened dystrophin encoding sequence.

Sequence 4402 BP; 1339 A; 984 C; 1010 G; 1069 T; 0 other;

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2071 CTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCTGG 2130
                                                                                                                                                        CAGGGTCCCTGGGAGAGACCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAG 1439
                                                                                                                                                                                                       CTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAG 1559
                                                                                                                                                                                                                                                                                                  GCCCTTTGCTTGGATCTCTTGAGCCTGTGGGTGCATGTGATGCCTTGGACCAGCACAAC 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A rod shortened dystrophin (deltaDysAx11) encoding nucleotide sequence.
                                               CTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTG 1259
                                                                                                                    GAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG 2190
                                                                                                                                                                                                                                          ACTCAAACAACTIGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTAGCTGAC 1499
                                                                                                                                                                                                                                                                                                                                                  CTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATT 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATAC 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATAC 2730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATT 2550
                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGACCGCCTGGAGCAAGAGCACAATTTGGTCAACGTCCCTCTCTGCGTGGATATG 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGCGCAGGCTGGGCCTCCTT 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1260 GAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAG
                                                                                                                                            TGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muscular dystrophy; rod domain; adeno-associated virus; AAV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ48567 standard; cDNA to mRNA; 4402 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2851 AACATTGAGCCAAGTGTCCGGA 2872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1980 AACATTGAGCCAAGTGTCCGGA 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ48567;
                                              1200
                                                                                                                                            1320
                                                                                                                                                                                                                 2251
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                                                                                                                                                                  2191
                                                                                                                                                                                          1380
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having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low immune reaction. The present sequence represents a rod shortened
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1255 GTATTATCGTGGCTTCTTCTGCTGACACATTGCAAGCACAAGGAGAGATTCTAAT 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1195 GGCAGTTCATTGATGGAGAGAGAAAACCTGGACCGTTATCAAACACTTTAGAAGAA 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1435 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1615 ACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGGACCTAAAACGCCCAAGTA 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a gene for the treatment of muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene encoding a shortened dystrophin - useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 4402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4402 BP; 1329 A; 1000 C; 1019 G; 1054 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                         (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.4%; Score 1269.2; 82.1%; Pred. No. 0;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 16-17; 44pp; Japanese.
            truncated; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dystrophin encoding sequence.
                                                                                                                                                                                                                                         98JP-0142134
                                                                                                                                                                                                                                                                                                98JP-0142134
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Matches 1644; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-100771/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscular dystrophy
dystrophin gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY59238
                                                                  Homo sapiens.
                                                                                                                   JP11318467-A
                                                                                                                                                                                                                                         08-MAY-1998;
                                                                                                                                                                               24-NOV-1999
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a ò	099	GAACAACITAAGGAGGICAAFACIGAGTGGGAAAA TGGGIICITITACAAGACAICCIICICAAAIGGGAACG	829
o qq	3		1 00
Qγ	720	TTTAGTGCATGGCTTTCAGAAAAAAAAAGATGCAGTGAACAAGATTCACACAACTGGCTTT	. ത
Db	1830		ω
οy	780	AAAGAICAAAAIGAAAIGTIAICAAGICTICAAAAACIGGCCGITTIAAAAGCGGAICIA 8	39
qq	1830		829
οy	840		66
qq	1830	1	829
λα	006	CŢ	59
QQ	1830	ATTGAACCTGCACTGACTGGCAGAGAA1	862
Oy Ph	960	TGGGATAATTTAGTCCAAAAACTTGAAAAGGTACAGCCAGACCCTTGAAAGACTCCAG	0.1
3	3		068
g ç	1020	GAACTTCAAGAGGCCACGGATGACTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAG 1 	079 950
op Op	1080	GGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGATCACCTCGAGAAA 	1139 2010
Q.Y	1140	GTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGAC 1 	199
7.7 Op	1200	CTG 1	259 130
Sy Ob	1260	t2 — t3	319 190
λα Q	1320	7	379 250
7.7 9.0	1380 2251	7 7	7
λζ	1440	-	Ō
q	2311		· -
2y qc	1500	CTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAG 1: 	559 430
λ ζ 90	1560	GCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAC 10	1619

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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, Hl and H4 domains and a cysteine rich domain of a
            TATGACCGCTGGAGCAGAGCACAAATTTGGTCAACGTCCCTCTCTGCGTGGATATG 1739
                                                                                                                                                                                                                      2790
                                                                                                          1920 CTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGT 1979
                                                                                                                                                                                                                                                       2791 CTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATTCTTGGGGGCAGT 2850
CICAAGCAAAAIGACCAGCCCAIGGAIAICCIGCAGAIIATIAAITGIIIGACCACTAII 1679
                                                                                                                                                                                             CITITICAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCAGGCTGGGCCTCCTT 1919
                                                                     2551 TATGACCGCCTGGAGCAAGAGCACAACTTTGGTCAACGTCCCTCTCTGCGTGGATATG
                                                                                              TGTCTGAACTGGCTGCTGAATGTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTG
                                                                                                                                                                                                          TCTTTTAAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 48-49; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human dystrophin minigene delta3849.
                                                                                                                                                                                                                                                                                                      2851 AACATTGAGCCAAGTGTCCGGA 2872
                                                                                                                                                                                                                                                                                            AACATTGAGCCAAGTGTCCGGA 2001
                                                                                                                                                                                                                                                                                                                                                                               AAD37237 standard; DNA; 3858 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-049342/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dystrophin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200183695-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (XIAO/) XIAO X.
                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                      AAD37237;
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                                               1680
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression

control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin miniqene delta3849 containing nucleotides 1-1668 (N·terminus, hinge HI and rods RI, R2), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

ж Э 1060 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 1119 GATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGA 1419 TTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCCGT 1779 1780 AAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGGAGCTGATGAAACAATGGCAAGAC 1839 1840 CTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAACAGCCAA 1899 1000 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCCTTTAGAAGAA 1059 240 360 629 719 539 ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 599 779 1 GGCAGTTCATTGATGGAGGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA 60 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTC GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 121 GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGGTACATGATGATTTGACA 181 GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA **AAATTATCAGAAGATGAAGAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA** TGGGAATGCCTCAGGGTAGCTAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATG GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAAGA **ACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTA** GAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGC TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTT TITAGTGCATGGCTTTCAGAAAAAGAAGATGCAGTGAACAAGATTCACACAACTGGCTTT TTAAAAGCGGATCTAGAAAAGAAAAGCAATCCATGGGCAAACTGTATTCACTCAAACAA A-------AAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTT Indels 412; DB 24; Length 3858; Sequence 3858 BP; 1189 A; 866 C; 905 G; 898 T; 0 other; 0; Mismatches 185; 63.1%; Score 1263; illarity 75.3%; Pred. No. 0; Conservative 0; Mismatches Best Local Similarity Matches 1816; Conserv Query Match 241 1240 1420 480 1480 540 1540 009 1720 61 099 720 301 361 g g ô q ò Db g g g 888888888 à g ö g ò g ŏ g ò δ ò à ò ò g

1448 1269 AACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGTGGAACTGGAA 1328 1509 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGC 1568 1569 TTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCACACCTCAAGCAA 1628 2020 GAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGTGG 2079 -----BGACCCTTGAAAGACTCCAGGAACTTCAA 1028 1029 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGG 1088 1089 CAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCA 1148 1900 AAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGAT 1959 1960 AACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCTCTCAACATTAGGTCCCATTTG 2019 2080 CTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACTTTGGAGGCGACTTTCCAGCA 2139 2140 GTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAAACTAAAGAACCT 2199 2200 GTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGA 2259 885 GATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAGACGGAAGCATGGCTGGAT 944 2440 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGG 2500 CAGCCCGTGGGCGATCTCCTCATGACTCTCTCCAAGATCACCTCGAGAAAGTCAGAGA 1449 ACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 945 AACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCAC----2320 ACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAATTGAACCTG 1149 CTTCGAGGAGAAATTGCGCCTCTGAAAGAGAGAACGTGAGCCACGTCAATGACCTTGCTCGC 2560 CTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGC 1209 CAGCTTACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG 2620 CAGCTIACCACTTTGGGCATTCAGCTCTCACCGTATAACCTCAGCACTCTGGAAGACCTG 2680 AACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAA 1389 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACA 2860 ACTIGCIGGGACCAICCCAAAAIGACAGAGCICIACCAGICITIAGCIGACCIGAAIAAI 2920 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGC 1000 -----1000 -----1000 q Ωp qq Dp q g Dp g ŏ qq δλ Qγ qq δy ò qq δy QΥ qq q ŏ q δy pp δ ò òγ δ δy δ δ δ ρý

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Query Match
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CTGGAGCAAGAGCACAACATTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTGTCTGAAC 3159
                                                                                                                                             TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTAAA 1808
                                                                                                                                                                                                ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 1868
                                                                                                                                                                                                                                                 1869 CAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGAT 1928
                                                                                                                                                                                                                                                                         3280 CAAGIGGCAAGIICAACAGGAITIIGIGACCAGCGCAGGCIGGGCCICCIICIGCAIGAI 3339
                                                                                                                                                                                                                                                                                                     TCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATTGAG 1988
                                                                                                                                                                                                                                                                                                                 3340 TCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATTGAG 3399
                                                               AATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGC
                                       AATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGC
                                                                                         Adeno-associated virus vector plasmid, AAV-MCK-delta3849
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD37257 standard; DNA; 4825.BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Becker muscular dystrophy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Homo sapiens.
Chimeric - Unidentified.
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AAD37257 RESULT

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4

Example 1; Page 61-62; 71pp; English.

dystrophin gene -

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a

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domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle
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                                                                                                                                                                                                                 creatine kinase (MCK) promoter and a small polyA signal sequence.
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                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 185; Indels 412;
                                                                                                                                                                                                                                                                                                                        DB 24; Length 4825;
                                                                                                                                                                                                                                                            Sequence 4825 BP; 1369 A; 1175 C; 1204 G; 1077 T; 0 other;
                                                                                                                                                                                                                                                                                               Score 1263;
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75.38;
                                                                                                                                                                                                                                                                                                                                                                   Matches 1816; Conservative
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                                                                         2657 AAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGAT 2716
                                                                                                                                        AACATGAACTTCAAGTGGAGTGAACTTCGGAAAAGTCTCTCAACATTAGGTCCCATTTG 2776
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                                            GATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAGACGGAAGCATGGCTGGAT
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New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
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                                        TIGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAA 3796
                                                                                                                                                CIGGAGCAAGAGCACAATTIGGICAACGICCCICTCTGCGTGGAIATGTGTCTGAAC 1748
                                                                                                                                                                                                                                                                     1809 ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 1868
                                                                                                                                                                                                                                                                                   1929 TCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATTGAG 1988
3677 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGC 3736
                                                                                     AATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGC 1688
                                                                                                                                                                                                                                                                                                                             1869 CAAGTGGCAAGTICAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGAT 1928
                                                                                                                                                                1917 TGGCTGCTGAATGTTTATGATACGGGACGACAGAGGAGGATCCGTGTCCTGTCTTTAAA
                           TIGGAICTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAACCTCAAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA; 4848
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    Cytomegalovirus.
    Unidentified.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4157 CCAAGTGTCCGGA 4169
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1989 CCAAGTGTCCGGA 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-049342/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dystrophin gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD37263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xiao X;
                                                                                                                                                                                                                                                                                                    3977
                               1569
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Example 1; Page 68-70; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a cytomegalovirus (CMV) promoter and a small polyA signal sequence.

X000000000000000

Sequence 4848 BP; 1405 A; 1144 C; 1180 G; 1119 T; 0 other;

Indels 412; Gaps Length 4848; 63.1%; Score 1263; DB 24; 75.3%; Pred. No. 0; 0; Mismatches 185; Best_Local Similarity 75.3 Matches 1816; Conservative Query Match Σ

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GGCAGTICATIGATGGAGAGTGAAGTAAACCTGGACGTTATCAAACAGCTTTAGAAGAA 1839 1 GCCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA 60 1780 ā

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ACTCACATGGTGGTGGTAGTTGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 540 2320

TGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGTCTTACTGAAGAACAGTGCCTT

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720 TITAGIGCAIGGCITICAGAAAAAAAAGAIGCAGIGAACAAGAIICACACAACIGGCIII 2500

780 A------AAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTT

ACTIGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 1508

3580

pp ò

1449

2560 AAGGAAAGGCTCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAAGAC 2619 2860 CTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCACCTATTGGAGGGGACTTTCCAGCA 2919 3100 ACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACTGAGTGGGAAAAATTGAACCTG 3159 TGGGAGAGAGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACTCAAACA 1448 TTAAAAGCGGATCTAGAAAAAGAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAACAA 2620 CTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAA 2680 AAAATCCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGAT 2800 GAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTTTCTCTGCAGGAACTTCTGGTGGG 3160 CACTCCGCTGACTGGCAGAGAAAATAGATGAGACCCTTGAAAGACTCCAGGAACTTCAA 3460 AACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAA GATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAGAGGGAAGCATGGCTGGAT 945 AACTITGCCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCAC----2920 GTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGGGAATTGAAAACTAAAGAACCT 2980 GTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTGACAGAGCAGCCTTTGGAAGGA 3040 CTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCTGAGGAGGAGAGCCCAGAATGTC -------AGACCCTTGAAAGACTCCAGGAACTTCAA 1029 GAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGG 1320 GAGGCCACGGATGAGCTGGACTCAAGCTGCGCCAAGCTGAGGTGATCAAGGGATCCTGG 1089 CAGCCCGTGGGCGATCTCCTCATTGACTCTCCCAAGATCACCTCGAGAAAGTCAAGGCA 1149 CTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGCCACGTCAATGACCTTGCTCGC 3340 CTTCGAGGAGAAATTGCGCCTCTGAAAGAACGTGAGCCACGTCAATGACCTTGCTCGC 1269 AACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTGCATGAA 885 1000 1000 1000 1000 1329 1389 1000 qq qq q δ Db ŏ Dp g Pp qq qq ð ŏ ŏ Óλ ô δ DB ò qq δ QQ Db g q Q δ δ Ω qq Ω

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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                   TCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGGCAGTAACATTGAG 1988
                                                                                                                                                                                                                              TGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCTTTAAA 1808
                                                                                                                                                                                                                                                                                     ACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTTTTCAAG 1868
                                                                                                                                                                                                                                                                                                                                                                                            CAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGGCCTCCTTCTGCATGAT 1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCAGTAACATTGAG 4179
                                                                                                                                                                                                             CTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGTGGATATGTGTCTGAAC 1748
                               1509 GTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGC 1568
                                                                                         1569 TTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCAGCACAAACCTCAAGCAA 1628
                                                                                                                                                  AATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGACCACTATTTATGACCGC 1688
3640 ACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTGAATAAT 3699
                                               Human dystrophin minigene delta3531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD37238 standard; DNA; 3531 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAGTGTCCGGA 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4180 CCAAGTGTCCGGA 4192
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                                                 The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a mammaliant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophin minigene delta3531 containing nucleotides 1-1341 (N-terminus, hinge H1 and rod R1), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1660 CGGAAAAAGTCTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAGCGT 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1360 TIACTGCAACAGITCCCCCTGGACCTGGAAAGITICTTGCCTGGCTTACAGAAGCTGAA 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1480 GGAGTAAAAGAGCTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACA 1539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1600 GATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTT 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1060 GTATTATCGTGGCTTCTTCTGCTGAGACACATTGCAAGCACAAGGAGAGATTCTAAT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1420 ACAACTGCCAATGTCCTACAGGATGCTACCGGTAAGGAAAGGCTCCTAGAAGACTCCAAG 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000 GGCAGTTCATTGATGAGAGAGAGAAAACCTGGACCGTTATCAAACGCTTTAGAAGAA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1300 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAACAAAGCAATTTACATAGAACTCATAGA 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 GAAAGAACAAGGAAAATGGAGGAAGACCTCTTGGACCTGATCTTGAAGACCTAAAACGC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GATCTCCAGAA-----TCGAAACTGAAAGATTGAATGACTGGCTAACAAAAACAGAA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTAGATGGACAGAAGACCGCTGGGTTCTTTACAAGACATCCTTCTCAAATGGCAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 CAAGTACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 TCTCTCACTCACATGGTGGTGGTAGTTGATGA-------ATCTAGTGGAGATCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 62.5%; Score 1251.2; DB 24; Length 3531; Best Local Similarity 77.8%; Pred. No. 0; Matches 1623; Conservative 0; Mismatches 378; Indels 85; 0
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3531 BP; 1071 A; 809 C; 824 G; 827 T; 0 other;
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                 Example 1; Page 50-51; 71pp; English.
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CTGCACCTTTCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGC 1779
                                                                                                          GCCTTCAAGAGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTA 1899
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                                                   CGGCAGGCACCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGG 1839
                                                                                                                                                               1900 CGAATATTTCTGACAGAGCAGCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGA 1959
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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is ANV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; dystrophin minigene; muscular; gene therapy; utrophin; spect adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
   CGAACAGGGAGGATCCGTGTCCTGTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCA
                       2860 CGAACAGGGAGGATCCGTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAAGCA
                                                                                              2920 CATTIGGAAGACAAGTACAGATACCTTITCAAGCAAGTGGCAAGTTCAACAGGATTTTGT
                                                                                                                                                   GACCAGGGCAGGCTGGCCTCCTTCTGCATGATTCTATCCAATTCCAAGACAGTTGGGT
                                                                          CATITICGAAGACAAGTACAGATACCTITITCAAGCAAGTGGCAAGTTCAACAGGATTTTGT
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                                                                                                                                                                                                                                             3040 GAAGTIGCATCCTTTGGGGGCAGTAACATTGAGCCCAAGTGTCCGGA 3085
                                                                                                                                                                                                                               GAAGTTGCATCCTTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adeno-associated virus vector plasmid, AAV-MCK-3531
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                                                                                                                                                                                                                                                                                                                                                           AAD37258 standard; DNA;
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Chimeric - Unidentified
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DB 24; Length 4498;

Score 1251.2; Pred. No. 0;

62.5%;

Query Match Best Local Similarity

Ma	atches	1623; Conservative 0; Mismatches 378; Indels 85; Gaps 6;	
Oy Dp	11757	GGCAGTTCATTGATGGAGAGTGAAGCTGGACCGTTATCAAACAGCTTTAGAAGA 60 	
Qy	61	GTATTATCGTGGCTTCTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTCTAAT 120	
QQ	1817	GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACACAGGAGAGAGTTTCTAAT 1876	
Oy Db	121	GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA 180 	
Oy Dp	181	GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240 	
δ da	241	AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGA 300 	
Qy Dp	301	360	
Qy Dp	361	GATCTCCAGAATCGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAA 413 	
Qy Db	414	GAAAGAACAAGGAAAATGGAGGAAGAGCTCTTGGACCTTGAAGACCTAAAACGC 473 	
Oy Dp	474	T 533	
Qy Dp	534	c 581 235	
Oy Dp	582 2357	GCAACTGCTGCTTTGGAAGAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATC 638	
oy Dp	639	TGTAGATGGACAGAGGCGCTGGGTTCTTTTACAAGACATCCTTCTCAAATGGCAACGT 698	
Oy Dp	699	CTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGAAAAAGAAGATGCAGTGAAC 758 	
Oy Dp	759	AAGATTCACACAAATGGGTTTAAAGATCAAAATGAAATG	
Oy Dp	819 2597	GCCGTTTTAAAAGCGGATCTAGAAAAGGAAAAGCAATCCATGGGCAAACTGTA 871 	
Qy Dp	872	TICACTCAAACAAGATCTTCTTCAACACTGAAGAATAAGTCAGTGACCCAGA 924 	
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οy	95	GTTGGGATATTTTAAAATTTGAAAAGGTGGA 995	
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                                                                                                GCACAGACCCTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAG
         CTGCGCCAAGCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGAC
                                          1116 TCTCTCCAAGATCACCTCGAGAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAA
                                                                          GCCGTCGAGGACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCCAGCATCT
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21-AUG-2002
AAD37230;
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Human dystrophin minigene delta4173.

Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.

Homo sapiens

WO200183695-A2

08-NOV-2001

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27-APR-2001; 2001WO-US13677

28-APR-2000; 2000US-200777P

(XIAO/) XIAO X.

WPI; 2002-049342/06

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a dystrophin gene -

Example 1; Page 43-44; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (BMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is human dystrophin minigene delta4173 containing nucleotides 1-1992 (N-terminus, hinge H1 and rods R1, R2 and R3), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).

Sequence 4182 BP; 1309 A; 927 C; 970 G; 976 T; 0 other;

2;

Indels 736; Gaps Length 4182; 62.2%; Score 1245; DB 24; 73.1%; Pred. No. 0; ive 0; Mismatches 0; Matches 2001; Conservative Local Similarity Query Match

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- 61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 120
- 121 GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGGATTTGACA 180

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- 181
- GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA 240

2320 TCTCTCAACATTAGGTCCCATTTGGAAGCCAGTTCTGACCAGTGGAAGCGTCTGCACCTT 2379

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2199	GAGCTGATGAAACAATGGCAAGACCTCCAAGGT	2140	Op
666		1000	Οy
2139	AATGTCCTACAGGATGCTACCCGTAAGGAAAGG	2080	qq
666	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1000	δλ
2079	CAGTTCCCCCTGGACCTGGAAAGTTT	2020	QQ
666		1000	δy
2019	TGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGGACAG	1960	qq
666	TGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCAC	096	Óλ
959 1959	CTGAAGAATAAGTCAGTGACCCAGAAGAGGGAAGCATGGCTG 	1900	QZ Dp
1899	GAAAAGAAAAGCAATCCATGGGCAAACTGTATTCACTC 	1840	QY Dp
839 1839	AAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTA 	780	Qy
779 1779	TTTAGTC TTTAGTC	720 1720	Oy Dp
1719		1660	Dp
9	GAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGA		Op
629	GAACAACTTAAAGGTATTGGGAGATCGGTGGGCAAACATCTGTAGATGGACAGAAGACGC	009	ΟY
1599		1540	a G
1539	CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCT	1480	QQ
539	CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAAT	480	Qγ
479	ACAAGGAAAAT ACAAGGAAAAT	1420	Oy Dp
419	GATCTCCAGAATC-GA	361 1360	DP CA
1359	TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAAT	ō	qq
360	. TGGGAATGCCTCAGGGTAGCTAGCATGGAAAACAAAGCAATTTACATAGAGTTTTAATG	301	δy

0y	1000	666	Φ.
QQ	2380	TCTCTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCA	39
Qy	1000	66	0
Dβ	2440	CCTATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAG 24	66
ογ	1000	66	6
Ωp	2500	AGGGAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATT 25	59
οy	1000	66	O
Dp	2560	CTGACAGAGCAGCCTTTGGAAGGACTAGAGAACTCTACCAGGAGCCCAGAGAGCTGCCT 26	19
οy	1000	66	on.
Ωp	2620	CCTGAGGAGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAAT 26	62
Ωÿ	1000	10 TO TO TO THE TOTAL THE TOTAL TO AL TO THE	04
QQ	2680	ACTGAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAAATAGATGAGACC 27	39
٥y	0	CTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAA 10	64
QQ	2740	CTTGAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAA 27	66
Oy Db	1065	GCTGAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTATTGACTCTCTCCAA 11:	24 59
٥y	1125	GATCACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTG 11:	
qq	2860		19
λο d	1185	AGCCACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGGCATTCAGCTCTCACGTAT 12.	44
3 2	, ,	01 040000000000000000000000000000000000	
op od	2980	ACCTCAGCACTCTGGAAGACTGAACACCAGATGGAAGCTTCTGGGTGGG	3.9
0y	30	GACCGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTT 13	
ga	0.4	GACCGAGTCAGGCAGCATGAAGCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTT 30	
Qy Db	1365	CTTTCCACGTCTGTCCAGGGTCCCTGGGAGAGCCATCTCGCCAAACAAA	2 4 59
Qγ	1425	TATATCAACCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGGGCTCTAC 14	84
Dp	3160		19
Qy Db	1485	CAGTCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTC 15	44
٥y	1545	CGAAGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCC 16	
QQ	3280		39
δŏ	9 6	TTGGACCAGCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAAT 16	
2	7	II BGACCAGCACACAICAACCAGAGAATGACCATGGATAICCIGCAGAITAITAAI 33	
y g	1665	TGTTTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAATTGGTCAACGTCCCT 17 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	24
δλ	72	CTCTGCGTGGATATGTGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGG 171	

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N terminal or modified N terminal domains, rod repeats, utrophin or a spectrin gene, HI and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammanlian subject. The present sequence is human dystrophin minigene delta3990 containing nucleotides 1-1668 (N-terminus, hinge H1 and rods R1 and R2), 8059-10227 (rods R22, R23 and R24, hinge H4 and CR domain) and 11047-11058 (dystrophin last 3 amino acids).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, H1 and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin;
adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD;
1905 AGGCTGGGCCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCA 1964
                                                                                                                                                                                                                3640 AGGCTGGGCCTCCTTCTGCATGTTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCA 3699
                                                                                                                          1845 GACAAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCCAACAGGATTTTGTGACCAGCGC 1904
                                                                                                                                             1785 AGGATCCGTGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAA
                                                                                                                                                                                                                                                                  Example 1; Page 46-47; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human dystrophin minigene delta3990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                               AAD37234 standard; DNA; 3999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-2000; 2000US-200777P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-049342/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dystrophin gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD37234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xiao X;
                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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Sequence 3999 BP; 1223 A; 907 C; 933 G; 936 T; 0 other;

Que Bess Mat Oy Oy Oy Oy	Ouery Match Best Local Similarity 71.1%; Score 1112; DB 24; Length 3999; Best Local Similarity 71.1%; Pred. No. 1.9e-312; Matches 1816; Conservative 0; Mismatches 185; Indels 553; GG 1 GGCAGTTCATTGATGGAGTGAAGTAAACCTGGACGGTATCAAACAGCTTTAGAAGAA	aps 60 10 12 11 11 11	.,	
2 A 2	81	24		
S 6	404	300		
Oy Dp	301 TGGGAATGCCTCAGGGTAGCTAGGAAAAAAAAACAATTTACATAGAGTTTTAATG 	360 1359		
Oy Db	361 GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAAGAAGAAGAAGA	419		
Qy	420 ACAAGGAAATGGAGGAAGCCTCTTGGACCTGATCTTGAAGACCTAAAAGGCCAAGTA 	479		
Qy Db	480 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTC	539		
Oy Db	540 ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA 	599 1599		
Cy c	600 GAACAACTTAAGGTATTGGGAGATCGGTGGGCAACATCTGTAGATGGACAGAAGACCGC	659		
Oy	660 TGGGTTCTTTTACAAGAC	77		
Qy		7.		
Db 1	1720 CCTACTCAGACTGTTACTCTGGTGACACAACCTGTGGTTACTAAGGAAACTGCCATCTCC	_		
Qy Db	678ATCCTTCTCAATGCCAACGT 1780 AAACTAGAAATGCCATCTTCTCTCTCTCTCAACGT	86		
Qy Db 1	699 CTTACTGAAGAACAGTGCCTTTTTAGTGCAGCAGGAAAGAAGAAGAAGAGGTGAACAGATTAGAGAAAGAA	758 1899		
Qy Db	L	03		
δy	AAAGCGGATCTAGAAAAGA	863		
Db 1	09	2019		
	864 AAACTGTATTCACTCAAACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAG	923		

qq	2020	
QY	924	AGCATGGCTGGATAACTTTGCCCGGTGTTGGGGATAATTTAGTCCAAAAACT
ОD	2080	CTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAAGTCT 2139
Qy	984	STACAG
qq	2140	CICAACAITAGGICCCAITIGGAAGCCAGITCIGACCAGIGGAAGCGICIGCACCITICI 2199
QY	1000	666
QQ	2200	CTGCAGGAACTICTGGTGTGGCTACAGCTGAAAGATGAATTAAAGCCGGCAGGCA
Qy	1000	666
QQ	2260	ATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGG 2319
Qy	1000	666
QΩ	2320	GAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTG 2379
QY	1000	666
QΩ	2380	ACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCT 2439
QY	1000	666
qq	2440	GAGGAGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACT 2499
Qy	1000	ACCCT
Dp	2500	GAGTGGGAAAAATTGAACCTGCACTCCGCTGACTGGCAGAGAAAATAGATGAGAGCCCTT 2559
Qy	1008	AAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTGCACCTGCGCCAAG
DP	2560	CAGGAACTICAAGAGGCCACGGATGAGC
Qy	1068	AGGTGATCAAGGGATCCTGGCAGCCGTGGGGGGATCTCCTCATTGACTCTCTCCAAGA
qa	2620	CCGTGGGCGA
Οy	1128	STGAG
qΩ	2680	AAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAGAGGAACG
Οy	1188	ACTITGGGCATICAGCICTCACCGTAT
Op	2740	CAATGACCTTGCTCG
Οy	1248	SGAAGCTTCTGCAGGTGGCCGTCGAGGA
DΒ	2800	
Qy	1308	CGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTT 1367
QQ	2860	SAGCAGCTGCATGAAGCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCT
Οy	1368	CATCTCGCCAAACAAAGTGCCCTACT
qq	2920	CCACGTCTGTCCAGGGTCCCTGGGAGAGAG
Qy	1428	CTACCA
qq	2980	SAACCAGAGACTCAAACAACTTGCTGGGACCA
Οy	1488	CTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCG
QQ	3040	ITAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAACT
Ολ	1548	AGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTG 1607

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The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteline rich domains of dystrophin or utrophin genes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, HI and H4 domains and a cysteine rich domain of a
                                                                                                                                                                                                                                                                              ATCCGTGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGAC 1847
                                                                                                                                                                                                                     AAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGG 1907
                                                                                                                                            TGCGTGGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGG 1787
3100 AGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTG 3159
                                                                                    TIGACCACTATITATGACCGCCTGGAGCAAGAGCACAACAATITGGTCAACGTCCCTCTC 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; dystrophin minigene; muscular; gene therapy; utrophin; spectadeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                     CIGGGCCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCC
                                                                                                                                                              3220 TTGACCACTATTTATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTC
                                                                                                     Adeno-associated virus vector plasmid, AAV-MCK-delta3990
                                                                                                                                                                                                                                                                                                                                                                             TTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGA 2001
                                                                                                                                                                                                                                                                                                                                                                                                          3520 TTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGA 3553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 59-60; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD37256 standard; DNA; 4966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-2000; 2000US-200777P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-2001; 2001WO-US13677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-049342/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dystrophin gene
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                                                                                         1668
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                                                                                                                                                                                                                                     3340
                                                                                                                                                                                                                                                                1848
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         comprising dystrophin minigene operably linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a muscle creatine kinase (MCK) promoter and a small polyA signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2477 CCIACTCAGACTGTTACTCTGGTGACACACCTGTGGTTACTAAGGAAACTGCCATCTCC 2536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2537 AAACTAGAAATGCCATCTTCCTTGATGTTGGAGGTACCTACTCATAGATTACTGCAACAG 2596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2237 CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAGTTCTCTC 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629
                                                                                                                                                                                                                                                                                                                                                   360
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                                                                                                                                                                                                                                                                               1757 GGCAGTTCATTGATGAGAGAGAGAAACCTGGACCGTTATCAAACAGGTTTAGAAGAA 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATCTCCAGAATC-GAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCTCTC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 ----- 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ATCCTTCTCAAATGGCAACGT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAAATTCAAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTA 479
                                                                                                                                                                                                                                                                                                                                61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                    121 GATGTGGAAGTGGTGAAAGACCAGTTTCATACTCATGAGGGGTACATGATGATTTGACA 180
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                              9
invention also relates to a recombinant adeno-associated virus (AAV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 ACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 GAACAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2417 TGGGTTCTTTTACAAGACCAGCCTGACCTAGCTCCTGGACTGACCACTATTGGAGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGAATGCCTCAGGGTAGCTAGCATGGAAAAAAAAGCAAATTTACATAGAGTTTTAATG
                                                                                                                                                                                                                                                             1 GGCAGITCATTGAIGGAGAGGTGAAGTAAACCTGGACCGTTATCAAACAGCTITAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGA
                                                                                                                                                                                                                             Indels 553;
                                                                                                                                                                                         Length 4966;
                                                                                                                                                          Sequence 4966 BP; 1403 A; 1216 C; 1232 G; 1115 T; 0 other;
                                                                                                                                                                                              DB 24;
                                                                                                                                                                                                         Pred. No. 2.1e-312;
0; Mismatches 185;
                                                                                                                                                                                           Query Match 55.6%; Score 1112; Best Local Similarity 71.1%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGTTCTTTTACAAGAC-----
                                                                                                                                                                                                                                 Matches 1816; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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qq	2597 T	TTCCCCCTGGACCTGGAAAAGTTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAAT 2656	
Qγ	759 4	AAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATG	
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Qy	804 A	AGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAGAAAAAAAA	
QΩ	2717 C	CTGATGAAACAATGGCAAGACCTCCAAGGTGAAATTGAAGCTCACACACA	
Oy Db	864 A	AAACTGTATTCACTCAAACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAG 923 	
δò	924 A		
qq			
δý	984 G	GAAAAGAGTACAGCAC 999	
οp	2897 C		
Qy	1000 -	666	
οp	2957 C	CTGCAGGAACTTCTGGTGTGGCTACAGCTGAAAGATGATTAAAGCCGGCAGGCA	
οy	1000 -	666	
QQ	3017 A	ATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGG 3076	
δÿ	1000 -	666	
qq	3077 G	GAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTG 3136	
οy	1000	666	
qq	3137 A	ACAGAGCAGCCTTTGGAAGGACTAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCT 3196	
٥y	1000 -	666	
qq	3197 G	GAGGAGAGAGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACT 3256	
Qγ	1000	1007	
qq	3257 G		
δλ		GAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCT 1067	
Dp	3317 G	AAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCCAAGCT 3376	
QY Dp	1068 G. 3377 G.	GAGGTGATCAAGGGATCCTGGCAGCCCGTGGGCGATCTCCTCATTGACTCTCTCCAAGAT 1127 	•
Qy H		CACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAGAG	
a .		accicgabaaagicaaggcacticgaggagaaaitgcgcctctgaaagagaaggggg 3496	
Qy Dp	1188 C	CACGTCAATGACCTTGCTCGCCAGCTTACCACTTTGGCCATTCAGCTCTCACCGTATAAC 1247 	
QY Db	1248 C	CTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGAC 1307 	<u> </u>
οy		136	
qq	3617 C	SAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTT 3676	-
Qy Dp	1368 TC 	TCCACGTCTGTCCAGGGTCCCTGGGAGAGCCATCTCGCCAACAAAGTGCCCTACTAT 1427 	

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Human; dystrophin minigene; muscular; gene therapy; utrophin; spectrin; adeno-associated virus; AAV; Duchenne muscular dystrophy; DMD; BMD; Becker muscular dystrophy; ds.
        1428 ATCAACCACGAGACTCCAAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAG 1487
                                                                  1548 AGACTGCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTG 1607
                                                                             1608 GACCAGCACAACCICAAGCAAAAIGACCAGCCCAIGGAIAICCIGCAGAIIAIIAAIIGI 1667
                                                                                                                                                                                                                                               1848 AAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGG
                                                                                                                                                                                                                                                                                   1908 CTGGGCCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                     Adeno-associated virus (AAV) vector plasmid, AAV-CMV-delta3990.
                                                                                                                                                                                                                                                                                                                              1968 TTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGA 2001
                                                                                                                                                                                                                                                                                                                                                                                 AAD37262 standard; DNA; 4990 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Homo sapiens.
Chimeric - Cytomegalovirus.
Chimeric - Unidentified.
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WPI; 2002-049342/06.

New dystrophin minigene for treating Duchenne or Becker muscular dystrophy comprises an N-terminal domain or modified N-terminal domain, rod repeats, HI and H4 domains and a cysteine rich domain of a dystrophin gene.

Example 1; Page 67-68; 71pp; English.

The present invention relates to an isolated nucleotide sequence encoding a dystrophin minigene. The minigene comprises N-terminal or modified N-terminal domains, rod repeats, utrophin or a spectrin gene, H1 and H4 domains and cysteine-rich domains of dystrophin or utrophin genes. The invention also relates to a recombinant adeno-associated virus (AAV) comprising dystrophin minigene operable linked to an expression control element. The dystrophin minigene in operable linkage with an expression control element, in a recombinant adeno-associated virus or retrovirus is useful for treating Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) in a mammalian subject. The present sequence is AAV vector plasmid construct containing human dystrophin minigenes, a cytomegalovirus (CMV) promoter and a small polyA signal sequence.

Sequence 4990 BP; 1439 A; 1185 C; 1208 G; 1158 T; 0 other;

Query Match 55.6%; Score 1112; DB 24; Length 4990; Best Local Similarity 71.1%; Pred. No. 2.1e-312; Matches 1816; Conservative 0; Mismatches 185; Indels 553; Gaps

4;

Matches 1816; Conservative U; Mismatches 185; Indels 553; Gaps

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QQ	2441	TGGGTTCTTTTACAAGACCAGCCTGACCTAGCTCCTGGACTGACCACTATTGGAGCCTCT 2500	_
Οy	678	249 613	
QQ	2501	CCTACTCAGACTGTTACTCTGGTGACACACACCTGTGGTTACTAAGGAAACTGCCATCTCC 2560	_
οy	678	ATCCTTCTCAAATGGCAACGT 698	
Db	2561	AAACTAGAAATGCCATCTTCCTTGATGTTGGAGGTACCTACTCATAGATTACTGCAACAG 2620	_
ζζ	699	CTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGAAAAAGAAGAAGATGCAGTGAAC 758	_
· ^0	75	AAGATICACACAACTGGCTTTAAAGATCAAAATGAAATGTTATCA 803	
DP -	8	 CCGTAAGGAAAGGCTCCTAG	_
δy	804	CATGGGC 863	
Dp	2741	GGTGAAATTGAAGCTCACACAGATGTTTATCA	_
Qy	864	AAACTGTATTCACTCAAACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAG 923 	_
Qy	924	AAGACGGAAGCATGCCTGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAAACTT 983	
Db	2861	CIGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTTCGGAAAAGTCT 2920	_
οy	984	GAAAAGACTACAGCAC 999	
qa	2921		_
οy	1000	666	
Db	2981	CTGCAGGAACTTCTGGTGGCTACAGCTGAAAGATGATGAATTAAGCCGGCAGGCA	_
δy	1000	666	
Db	3041	ATTGGAGGCGACTTTCCAGCAGTTCAGAAGCAGAACGATGTACATAGGGCCTTCAAGAGG 3100	_
ΟY	1000	666	
Db	3101	GAATTGAAAACTAAAGAACCTGTAATCATGAGTACTCTTGAGACTGTACGAATATTTCTG 3160	0
Qγ	1000	666	
Dp	3161	ACAGAGCAGCCTTTGGAAGGACTAGAGAAACTCTACCAGGAGCCCAGAGAGCTGCCTCCT 3220	0
٥y	1000	666	
pp	3221	GAGGAGAGGCCCAGAATGTCACTCGGCTTCTACGAAAGCAGGCTGAGGAGGTCAATACT 3280	0
Qy	1000	1007 1007 1007 1007 1007 1007 1007 1007	7
qa	3281	GAGTGGGAAAAATTGAACCTGCACTCGCTGACTGGCAGAGAAAATAGATGAGACCCTT 3340	0
ΟY	1008	GAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCAAGCTGCGCCAAGCT 1067	7
qq	3341	GAAAGACTCCAGGAACTTCAAGAGGCCACGGATGAGCTGGACCTCCAAGCTGCGCCAAGCT 3400	0
δŽ	1068		7
Dp	3401	T 346	0
VQ 4	1128	CACCTCGAGAAAGTCAAGGCACTTCGAGGAGAAATTGCGCCTCTGAAAGAGAACGTGAGC 1187 	2 2
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CTCAGCACTCTGGAAGACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGAC 1307
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1367 CGAGTCAGGCAGCTGCATGAAGCCCACAGGGACTTTGGTCCAGCATCTCAGCACTTTCTT qq ŏ

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1428 ATCAACCACGAGACTCGAACAACTTGCTGGGACCATCCCCAAAATGACAGAGCTCTACCAG 1487

1488 TCTTTAGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGA 1547

GACCAGCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGT 1667 1608

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TIGACCACTATITATGACCGCCTGGAGCAAGACACAAATTTGGTCAACGICCCICIC 1727 TGCGTGGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAACGGGAGG 1787. 1668 1728

AAGTACAGATACCTTTTCAAGCAAGTGGCCAAGTTCAACAGGATTTTGTGACCAGCGCAGG 1907 1848

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Search completed: April 25, 2003, 08:47:15 Job time : 384.185 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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BB627285 BB627285
AI196693 ui53e10.y
BF182065 601804604
BB666688 BB666688
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AL672616 AL672616
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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VERSION
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AUTHORS
TITLE
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SOURCE
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AL556247
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ORIGIN

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enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URA. : http://fulllength.invitrogen.com"
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Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 620)
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Homo sapiens cDNA clone he23g04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    1433 CCACGAGACTCAAACAACTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTT 1492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 TGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 547
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100.0%; Pred. No. 3.8e-129;
:ive 0; Mismatches 0;
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splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), (2002) In press
Contact: Wistow G
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                                                                                                                         Section on Molecular Structure and Function
National Eye Institute
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                                                                                                                                                                                                                                                                                                                                Email: graeme@helix.nih.gov
Plate: 23 row: g column: 04
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                       6/331, NIH, Bethesda, MD 20892-2740,
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="EMDH10B"
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (strain:C57BL/6J) adult male hippocampus cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2900010C03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus adult male hippocampus CDNA, RIKEN full-length enriched library, clone:2900010C03:dystrophin, muscular dystrophy, AK013510
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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                                                                                                                                                                                                            450 GTGGATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATC 509
                                     330 GCACAATCCTCAAGTCAGAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTG 389
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               Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
http://image.llnl.gov
Plate: LLAMI0731 row: 1 column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                          602690430F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4822807 5',
1924 ATGATICTAICCAAATICCAAGACAGIIGGGGGAAGIIGCAICCITIGGGGGCAGIAACA 1983
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                         1 (bases 1 to 770)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_97"
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Location/Qualifiers
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98.1%;
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Larloan, Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adakawa, Y., Baldarelli, R., Bono, H., Browstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Nimazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owacken, Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrind, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasuishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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Submitted (10.50L-2000) Yoshihide Hayashizaki, The Institute of Submitted (10.50L-2000) Yoshihide Hayashizaki, The Institute of Exploration and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, NRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="hippocampus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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124. .900
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/uc_all in MEHICAGE TOTACWDHPKWTELYQSLADLNNVRFSAYRTAMKL RRLQKALCLDLLSLSAACDALDQHNLKQNDQPWDILQIINCLTTIYDRLEGEHNNLVN VPLCVDMCLWULNVYDFGRTGRIRVLSFKYGIISLCKAHLEDKYRYLEKQVASSTGF CDQRRLGLLLHDSIQIPRQLGEVAFFGSNIEPSVRSCFQFANNKPEIEAALFLDWMR LEPQSHVWLPVLHRVAAATTAKHQAKCNICKECPIIGFRY"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/note="data source:MGD, source key:MGI:94909,
                                                                                                                                                                                                                                                                                                                                   36; Indels
                                                                                                                                                                                                                                                                                            Score 511.4; DB 11;
Pred. No. 7.6e-115;
                                    dystrophin, muscular dystrophy
                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                      /protein_id="BAB28887.1"
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                                                                         /codon_start=1
                     evidence: ISS
                                                                                                                                                                                                                                                                                              Query Match 25.6%;
Best Local Similarity 93.7%;
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hayashizaki,Y.
hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
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                                                                                                                                                     1433 CCACGAGACTCCAAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1492
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                                                               24.7%; Score 494.6; DB 10, 93.0%; Pred. No. 7.5e-111;
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Contact: Yoshihide Hayashizaki
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//dev_stage="10 day old"
//dev_stage="10 day old"
//note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn overy cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y. and Hayashizaki,Y.
Computer-Dased methods for the mouse full-length CDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. .10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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                                                                                                                Email: genome res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carnindi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carnindi,P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
perpare full-length cDNA libraries for rapid discovery of new
aggi,K., Fujiwake,S., 10(10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Mattahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810074E05"
/clone="lib="RIKEN full-length enriched, 10 day old male pancreas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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FEATURES

1433 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1492

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ORIGIN

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A1196693 854 bp mRNA linear EST 14-OCT-1998 u153810.91 Sugano mouse liver mlia Mus muscutlus CDNA clone IIMAGE:1886154 5' similar to gb:M18533 DYSTROPHIN (HUMAN); gb:M68859 Mouse dystrophin mRNA, exons 1-7 and complete cds (MOUSE);, mRNA
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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This clone is available royalty-free through LLNL ; contact the
IMAGE_Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Washington University School of MedicineP
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Contact: Marra M/Mouse EST Project
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High quality sequence stop: 460.
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/note="Organ: liver; Vector: pWE18S-F13; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTAGTGG], digested
and cloned into distinct DraIII sites of the pME18S-F13
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTGTCTGTTAAAAGGTGCG and 3' end
primer CGACCTGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1433 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 ccagaaggcccrrrgcarcrcrrgagccrgrcagcrgcargrgargccrgaacca 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.3%; Score 467.2; DB 9; Length 854; 90.9%; Pred. No. 4.5e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                   3 others
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                                                      /clone_lib="Sugano mouse liver mlia"
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0; Mismatches 50;
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                   /db_xref="taxon:10090"
/clone="IMAGE:1886154"
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                                                                                                  /dev_stage="adult"
/lab_host="DH10B"
/strain="C57BL"
                                                                            /sex="female"
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Matches 518; Conservative
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EST 31-OCT-2000

linear

mRNA

868 pb

601804604F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4035505 5',

mRNA sequence. BF182065

DEFINITION

LOCUS

RESULT 8 BF182065

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7;
                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1433 CCACGAGACTCAAAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1492
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                                                                                                                                                                NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1729 GCGTGG-ATATGTGTCTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGG 1787
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ches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:4035505"
/clone_lib="NOI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH108"
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                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"/strain="C57BL/6J"
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High quality sequence stop: 675.
Location/Qualifiers
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                    BF182065.1 GI:11060207
                                                                                                                                                   (bases 1 to 898)
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                                                                                                                                                                                                               Unpublished (1999)
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                                                              house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                               BB666688 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330026B12 5', mRNA sequence.
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URL:http://genome.go.gr.riken.go.jp,
URL:http://genome.go.gr.riken.go.jp,
Carninci.p., Shibata,Y., Hayasu.N., Sugahara,Y., Shibata,K., Itoh
A., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
appense. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshinde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 599)
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1848 AAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGG 1907
                                                                                                                           1908 CTGGGCCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCC 1967
                                                                                                                                                               548 AAGTACAGATACCTTTTCAAGCAAGTGGCAAGTTCAACTGG-TTTTGTGAGCAGCGTAGG 606
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                                1968 TTTGGGGGCAGTAACATTGAGCCAAGTGTCCGGA 2001
                                                                                                                                                                                                                                                                                          1 .599
/organism="Mus musculus"
/db_xref="taxon:10090"
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COMMENT

ACCESSION VERSION KEYWORDS

SOURCE

BB666688 RESULT 9

LOCUS

REFERENCE

source

FEATURES

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Homo.sapiens, dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS272, clone IMAGE:3029414, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                       prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                 /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 161 c 142 g 150 t
/clone="E330026B12"
/clone_lib="RIKEN full-length enriched, 2 days pregnant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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93.3%; Pred. No. 3.9e-90;
w.cmatches 31; Indels
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                                                                                                       /tissue_type="ovary"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       557 CAGATACCTTTTCAAGCAAGTGGCAAGTTCACTGGCTTTT 596
                                                                                                                                                                                                                                                                                                                                              primed with a primer [5'
                                                    female ovary"
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BC009242.1 GI:14714379
                                                                             /sex="female"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5032280
This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                      contact; amadanesystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                Submitted (06-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1069 GGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGTTTAGAAGAA 1128
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                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                     Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 402.6; DB 11; Length 1490;
Pred. No. 4.1e-88;
0; Mismatches 4; Indels 1;
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/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens/db_xref="LocusID:1756"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:3029414"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pOTB7"
299 c 328 g
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98.8%;
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AL641565 AGC-neurula Silurana tropicalis cDNA clone TNeu012d20 5',
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1433 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu012d20.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 385.2; DB 9; Length 684;
Pred. No. 6.3e-84;
                                                                                                                                                                                                                                        Xenopodinae; Silurana.

1 (bases 1 to 684)

Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Ro.
Sanger Xenopus tropicalis EST project 2001 (10_2001)

Contact: Huckle E
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .684
/organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                      Hinxton, Cambridgeshire, CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="XGC-neurula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:8364"
/clone="TNeu012d20"
                                                                                          AL641565.1 GI:16793690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.3%;
84.7%;
                                                                                                                                           western clawed frog
                                                                                                                                                                        Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 432; Conservative
                                              mRNA sequence.
AL641565
                                                                                                                                                                                                                                                                                                                                                                                            Sanger Centre
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AL641565
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(bases 1 to 423)
Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, Y., Washu Marck EST Project 1997,
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                             EST 09-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                AA460476 423 bp mRNA linear EST 09-JUN-1
zx61e10.rl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:795978 5' similar to gb:M18533 DYSTROPHIN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is avallable royalty-free through LLNL; contact the
This clone is avallable royalty-free through LLNL; contact the
This clone is avallable royalty-free through LLNL; contact the
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 287.
Location/Qualifiers
                                                                                           1853 CAGATACCTTTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGCGCAGGCTGGG 1912
1793 TGTCCTGTCTTTTAAAACTGGCATCATTTCCCTGTGTAAAGCACATTTGGAAGACAAGTA 1852
                                           535 CGTCTTATCTTTTAAAACTGGTGTAATTTCCCTGTGTAAAGCACATTTGGAAGATAAGTA 594
                                                                                                                                           595 CAGATACTTATTCAAGCAGGTGGCAAGCTCCACGGGATTCTGTGACCAGCGGAGACTGGG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/organism="Homo sapiens"
/db_xref="texon:9605"
/db_xref="texon:9605"
/db_xref="texon:9606"
/clone="INAGE:795978"
/clone="INAGE:795978"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 381.8; DB 9;
Pred. No. 3.8e-83;
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                                                                                                                                                                                                                    655 CCTGCTTTTACATGCAATTCAAATTCC 684
                                                                                                                                                                                                                                                                                                                                                             423 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA460476.1 GI:2185222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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JOURNAL
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AUTHORS
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AL796733 XGC-neurula Silurana tropicalis cDNA clone TNeu143c03 5',
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/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taylor, R., Abhurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
Contact: Taylor R
Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1433 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1492
1493 AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 1552
                                                                                     1553 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGCCTTGGACCA 1612
                                                                                                                                                                              1613 GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1672
                                                                                                                                                                                                                                                                    1673 CACTATTTATGACCGCCTGGAGCAAGAGCACAACTTTGGTCAACGTCCCTCTCTGCGT 1732
                                                                                                                                                                                                                                                                                                                                                          1733 GGATATGTGTCTGAACTGGCTGCTGAAT-GTTTATGATACGGGACGAACAGGGAGGATCC 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 CCATGAGACACACACCTGCTGGGATCATCCCAAAATGACAGAATTATATACCAATCTTT 172
                                                                                                                                                                                                                                                                                                                                                                                 147 GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCATGTGATGTCTTGGACCA 206
                                                                                                                                                                                                                                                                                                             326
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Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu143c03.plcSP6
Sequencing primer: PICSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.0%; Score 380.4; DB 9; Length 633; 84.3%; Pred. No. 9.4e-83; ive 0; Mismatches 81; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1792 GIGICCIGICITITAAAACIGGCAICATITCCCIGIG 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 GIGTCCTGTCTTTTAAAACCGGCATCATTTCCCTGTG 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="XGC-neurula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:8364"
/clone="TNeu143c03"
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1 (bases 1 to 633)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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JOURNAL
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Gaps

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Indels

Length 423;

1433 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 1492

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Conservative

Matches 394; Query Match Best Local 9

Similarity

19.18; 99.28;

27 CCACGAGACTCAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTT 86

/clone_lib="Zebrafish Research Genetics C32 fin"

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EST 30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 665)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S.L., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ### 1103h06.x1 Zebrafish Research Genetics C32 fin Danio rerio cDNA 3/ similar to TR:Q02295 Q02295 MAJOR DUCHENNE MUSCULAR DYSTROPHY PROTIEIN; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome
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                                                                                                                                                           GCACAACCTCAAGCAAAATGACCAGCCCATGGATATCCTGCAGATTATTAATTGTTTGAC 1672
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  AGCTGACCTGAATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACT 1552
                                                                              GCAGAAGGCCCTTTGCTTGGATCTCTTGAGCCTGTCAGCTGCGTGTGATGCCTTGGACCA 1612
                                                                                                                                                                                                                                                          CGTCTTATCTTTTAAAACTGGTGTAATTTCCCTGTGTAAAGCACATTTGGAAGATAAGTA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
Research Genetics. DNA Sequencing by: Washington University
Sequencing Center Clone distribution: Research Genetics web
address: http://www.researchgenetics.com/
Seg primer: T7 FT from Annersham
High quality sequence stop: 497.
Location/Qualifiers
                      GCACAACCTGAAGCAGAATGACCAGCTGATGGACATCCTGCAGATTATTAATTGCTTGAC
                                                                                                                                                                                                                                         CACTATITATGACCGCCTGGAGCAAGAGCACAACAATTTGGTCAACGTCCCTCTCTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contract: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCCTTCTGCATGATTCTATCCAAATTCCAAGACAGTTGGG 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU Zebrafish EST Project 1998
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:8714147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio
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BE201973.1
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BE201973/c
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DEFINITION
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VERSION
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COMMENT
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/organism="Danio rerio" /db_xref="taxon:7955"

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                                                                              Site_1: ECORI; Site_2: NotI; 1st strand coDA was prepared from zebrafish(C32) fin, and was then primed with a Not I -0190(dT) primer. Double-stranded coDA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library is non-normalized. Library was constructed by Ning Wu. NOTE: Clones from this library are only available thru Research Genetics (www.resgen.com)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2334)
                   /lab_host="GeneHogs (HS996, a phage-resistant isolate of DH10B)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1875 GCAAGITCAACAGGAITTTGIGACCAGCGCAGGCIGGGCCICCTICTGCATGAITCIAIC 1934
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                                                               /note="Vector: pT7T3D-Pac with a modified polylinker;
                                                                                                                                                                                                                                                                                                                                                                                                                                             665 TGGGGACACCCAAAGATGNCAGAACTCTACCAGTCATTAGCGGATCTCAACAACATGGGG 606
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Mus musculus, Similar to utrophin, clone IMAGE:3979320, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1515 TTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCCCTTTGCTTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found
                Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov
Series: TRAK Plate: 23 Row: J Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis. Similarity but not identity to protein
This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                           Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1402 CTGCAGAAGAAGAGCTGCAGCAGCTGCTCAAGCTGGCCCCTCACAGAAGAGCGCCTT 1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam1"
/lab_host="DH10B"
                                                                                                                                                  Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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59.0%; Pred. No. 7.8e-71;
tive 0; Mismatches 409;
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/organism="Mus musculus"
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  Strausberg, R.
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ORIGIN
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AUTHORS
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1702 AACAGGTTGCAAGAAATCAGTATTCTGTGGCAGGAATTATTGGAAGAGCAGTGTTGTTG 1761
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423 AGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAA 482
                                                                                                                                                                                                                                    CACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAA 602
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                                                                                                                  CAACTTAAGGTATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGG
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Sequence 9, Appli
Sequence 10, Appli
Sequence 13, Appli
Sequence 12, Appl
Sequence 447, Appli
Sequence 4, Appli
Sequence 212, Appli
Sequence 213, Appli
Sequence 236, Appli
                                                                                                                                                                                                 (without alignments)
13465.096 Million cell updates/sec
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Appl
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                                                                                                                                                                April 25, 2003, 08:10:12 ; Search time 45.5741 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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	ALIGNMENTS						
Sequence 193, App	US-08-630-915A-193	4	2873	1.7	34	45	
Sequence 2, Appli	US-09-153-804-2	4	2235	1.7	34	C 44	
Sequence 3, Appli	US-09-244-796-3	4	277	1.7	34	43	
Sequence 3, Appli	US-09-007-005-3	4	277	1.7	34	42	
Sequence 32, Appl	US-09-244-796-32	4	248	1.7	34	41	
Sequence 32, Appl	US-09-007-005-32	4	248	1.7	34	40	
Sequence 3, Appli	US-09-747-116-3	4	2800	1.7	34.2	39	
٦,	US-09-747-116-1	4	2800	1.7	34.2	38	
'n	US-08-879-941-3	4	2800	1.7	34.2	37	
Sequence 1, Appli	US-08-879-941-1	4	2800	1.7	34.2	36	
Sequence 5, Appli	US-08-874-138-5	7	2800	1.7	34.2	35	
Sequence 1, Appli	US-08-874-138-1	7	2800	1.7	34.2	34	
Sequence 56, Appl	US-08-858-207A-56	4	1620	1.7	34.2	33	
Sequence 204, App	US-09-328-111-204	4	621	1.7	34.2	c 32	
Ω,	US-09-098-487-5	~	2277	1.7	34.6	c 31	
Sequence 5, Appli	US-08-676-974-5	Н	2277	1.7	34.6	c 30	
Sequence 5, Appli	US-08-676-967-5	Н	2277	1.7	34.6	c 29	
Sequence 997, App	US-09-134-001C-997	4	366	1.7	34.8	28	

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2056 CAAGAAATCAAATTTTTGAAAAATTCAATTAAAAAGACAGATGGGGAATGTGTTTA 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 GTTGGTAATATCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGAT 255
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Pred., No. 0.011;
0; Mismatches 126; Indels 0
                                                                               APPLICANT: RUYKUN, Gary
APPLICANT: RUYKUN, Gary
APPLICANT: Patrerson, Garth
APPLICANT: Patrerson, Garth
APPLICANT: Paradis, Suzanne
APPLICANT: Paradis, Suzanne
APPLICANT: Paradis, Suzanne
APPLICANT: Howeek, Allison
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: THAPIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351001
CURRENT APPLICATION NUMBER: US/08/857,076C
CURRENT FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSEQ for Windows Version 4.0
                      Sequence 44, Application US/08857076C Patent No. 6225120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Caenorhabditis elegans
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48.48;
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Best Local Similarity 48.48
Matches 118; Conservative
                                                               GENERAL INFORMATION:
-08-857-076-44/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALARIA RECOMBINANT POXVIRUS VACCINE
                                                                                                                                                                                                                                              APPLICANT: MOTION: Jason
APPLICANT: KOWEEK, Allison
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/331001
CURRENT APPLICATION NUMBER: US/08/857,076C
CURRENT FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08257073
Patent No. 5765697
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIR
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNITED STATES OF AMERICA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                       Sequence 43, Application US/08857076C Patent No. 6225120 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Caenorhabditis elegans US-08-857-076-43
                                                                                             APPLICANT: Ruvkun, Gary
APPLICANT: Kimura, Koutarou
APPLICANT: Patterson, Garth
APPLICANT: Ogg, Scott
APPLICANT: Paradis, Suzanne
APPLICANT: Tissenbaum, Heidi
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JS-08-857-076-43/c
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428 AATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACA 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%; Score 39.4; DB 1; Length 2223; Best Local Similarity 51.4%; Pred. No. 0.086; Matches 91; Conservative 0; Mismatches 86; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09007005B
Patent No. 625858
GENERAL INFORMATION:
GENERAL SEOSTAK, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: ELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 60/035,963 EARLIER FILING DATE: 1997-01-27 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                             NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
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                CLASSIFICATION: 424
                                                                                                                                 APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELET: 42506 CURINS
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                  FILING DATE: 20-MAR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 17
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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1453 AAAACTAAAACCTTTTCAGCAACAACTGGATGCCTTTGAAGCCGAGAAACAGGCATTGTTG 1512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 AAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCGAAACTGAAAGAGTTG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 ACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAACTGAAGT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 NRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNR 131
                                                                                                          132 NRSKNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRN 191
                                                                                                                                                                                             192 NRSRNRNRSRNRNRSRNRNRSRNRNRSRCRARGRCRGRGRARARGRURGR 251
                                                         469 AACGCCAAGTACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGG
                                                                                                                                                                529 TCAATTCTCTCACACCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTG
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DESCRIPTION: /desc = "RHAMM I cDNA (coding region)"
US-08-477-831C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.9%; Score 38.8; DB 4; I larity 48.0%; Pred. No. 0.12; Conservative 0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TURLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
WUMBER OF. SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...ocf1
...ock: US/08/477,831C
07-JUN-1995
JN: 514
TNIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: FISH & NEAVE
STREET: 1251 AVENUE OF THE AMERICAS
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
FORMATION: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08477831C Patent No. 6429291 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             589 CTGCTTTGGAAGAACAACTTAA 610
                                                                                                                                                                                                                                                                                                                                 252 GRCRGRCRUAAAAAAAAAAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: PIERI, MARGARET A.
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1821 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic STRANDEDNESS:
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Best Local Simi
Matches 142;
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                                                                                                                                                                                                                                                                                                                                                                                                   72 NRSKNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 NRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 NRSRNRNRSRNRNRSRNRNRSRCRNRRRGRCRURGRCRGRARARCRURGR 251
                                                                                                                                                                                                                                                    349 AGAGTTTTAATGGATCTCCAGAATCGAAACTGAAAGGGTTGAATGACTGGCTAACAAAAA 408
                                                                                                                                                                                                                                                                                                                                                              409 CAGAAGAAAGAACAAGGAAAATGGAGGAAGAAGACCTCTTGGACCTGATCTTGAAGAACTTAA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 AACGCCAAGTACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGG 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 TCAATTCTCTCACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTG 588
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                                                                                                                                                                                                                                                                                                       12 ARARURURARCRURARURURURURARCRARARURURARCRARARURGRNRNRSRNRNRSRNR 71
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Patent No. 6281344

GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Liu, Rihe
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: UNMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER FILING DATE: 1999-02-05
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER PETING DATE: 1998-01-14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.9%; Score 38.8; DB 4; Length 289; Best Local Similarity 8.8%; Pred. No. 0.032; Matches 23; Conservative 104; Mismatches 135; Indels
                                                                                                                                            Length 289;
                                                                                                                                                                                                Indels
                                                                                                                                      Query Match 1.9%; Score 38.8; DB 4; Best Local Similarity 8.8%; Pred. No. 0.032; Matches 23; Conservative 104; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : LOCATION: (1)...(289)
: OTHER INFORMATION: n = A,T,C or G
JS-09-244-796-17
  NAME/KEY: misc_feature
LCCATION: (1)...(289)
CTHER INFORMATION: n = A,T,C or G
S-09-007-005-17
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TYPE: RNA

450 CCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCAAGAAGA 505

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1513 AATGAACATGGTGCAACTCAGGAGCAGCTAAATAAAATCAGAGACTCCTATGCACAGCTA 1572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1577 AATGAACATGGTGCAACTCAGGAGCAGCTAAATAAAATCAGAGACTCCTATGCACAGCTA 1636
390 AATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 ACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGATGAAGAAACTGAAGT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 AAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCGAAACTGAAAGAGTTG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 AATGACTGGCTAACAAAAAAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                    450 CCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCAAGAAGA
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                                                                                                                                                                                                                                                                                                                 APPLICANT: TUREEY, EVA A.
APPLICANT: TUREN, ZHANG
APPLICANT: SHUWEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TILLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rel. #1.0, ASCII
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/477,831C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: FISH & NEAVE
1251 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;: DESCRIPTION: /desc = "RHAMM IB"
US-08-477-831C-9
                                                                                                                                                                                                                                                      Sequence 9, Application US/08477831C Patent No. 6429291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PIERRI, MARGARET A.
REGISTRATION NUMBER: 30,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: SI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-556-9000
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-550-5000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1885 basirs
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Best Local Similarity 48.09
Matches 142; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 10020-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                 US-08-477-831C-9
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                                                                                                                                                                                                         RESULT 7
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1470 GACAGAATTAACCATGGAAATTAAT -- AAATGGCGTCTCCTATATGATGAACTATATGAA 1527
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450 CCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCAAGAAGA 505
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48.0%; Pred. No. 0.12;
tive 0; Mismatches 152; Indels 2
                                                                                                                                                                                                                                                                                    Parent No. 6429291
GENERAL INFORMATION:
APPLICANT: TURLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1251 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Rel. #1.0, ASCII
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,831C
FILING DATE: 07-JUN-1995
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DESCRIPTION: /desc = "RHAMM I-2a"
                                                                                                                                                                                                                                            Sequence 10, Application US/08477831C Patent No. 6429291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STALL.
COUNTRY: U.S.A..
ZIP: 10020-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TYPE: IBM PC COMPALIBLE
TYPER: IBM PC COMPALIBLE
TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: TYPER: 
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REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIN
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TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 48.09
Matches 142; Conservative
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STRANDEDNESS: sing
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: U.S.A.
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                                                                                                                                                                                                        US-08-477-831C-10
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1593 AAAACTAAAACCTTTTCAGCAACAACTGGATGCCTTTGAAGCCGAGAAACAGGCATTGTTG 1652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9%; Score 38.8; DB 4; Length 1961;
48.0%; Pred. No. 0.12;
tive 0; Mismatches 152; Indels 2;
                                                                   GENERAL INFORMATION:
APPLICANT: TURLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                  ...ock: US/08/477,831C
07-JUN-1995
NI: 514
                                                                                                                                                                                                            ADDRESSEE: FISH & NEAVE
STREET: 1251 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Rel. #1.0, ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIM-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
DESCRIPTION: /desc = "RHAMM IA"
                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                             Sequence 8, Application US/08477831C Patent No. 6429291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEPRAX: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                     1: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: EDNGTH: 1961 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: PIERRI, MARGARET A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                          RY: U.S.A.
10020-1104
                                                                                                                                                                                                                                                                           NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                  CITY: NEW YORK
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                                                                                                                                                                                                                                                                                          COUNTRY:
              -08-477-831C-8
                                                                                                                                                                                                                                                                           STATE:
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ESULT 9
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1517 AAAACTAAACCTTTTCAGCAACAACTGGATGCCTTTGAAGCCGAGAAACAGGCATTGTTG 1576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA DESCRIPTION: /desc = "RHAMM IB cDNA (includes 3' sequence)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.0%; Pred. No. 0.16;
Matches 142; Conservative 0; Mismatches 152; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TURLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: BATWISTLE, JOYCELYN
APPLICANT: BATWISTLE, JOYCELYN
APPLICANT: BY HYSLURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
APPLICANT: TURLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
UNBARE OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Rel. #1.0, ASCII
CURRENT APPLICATION DATA:
                                                                                                                                          ADDRESSEE: FISH & NEAVE STREET: 1251 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/477,831C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATORNEY/AGRY INFORMATION:
NAME: PIERRI, WARGARET 30,709
REFERENCE/DOCKET NUMBER: SIM-10
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08477831C Patent No. 6429291
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2968 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                  NEW YORK
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                                                                                                                                                                                          NEW YORK
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NUMBER OF SEQ ID NOS: 5674
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                               US-09-134-001C-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                   SEQ ID NO 447
LENGTH: 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
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GENERAL INFORMATION:

APPLICANT: Lynn boucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1535 GACAGAATTAACCATGGAAATTAAT--AAATGGCGTCTCCTATATGATGAACTATATGAA 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1653 AATGAACATGGTGCAACTCAGGAGCAGCTAAATAAAATCAGAGACTCCTATGCACAGGTA 1712
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Best Local Similarity 48.0%; Pred. No. 0.17;
Matches 142; Conservative 0; Mismatches 152; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 CCTGATCTTGAAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCAAGAAGA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
DESCRIPTION: /desc = "RHAMM IA CDNA (includes 3' sequence)"
                  ADDRESSEE: FISH & NEARLY STREET: 1251 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel. #1.0, ASCII CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/477,831C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
COMPUTER: PC COMPATIBLE
COMPUTER: PC COMPATIBLE
COMPUTER: PC COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PIERRI, MARGARET A.
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHRRACTERISTICS: LENGTH: 3044 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                         STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10020-1104
COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                               207 AGTIGAAATITTICICAATAATCACTITTATCGITAAAAGTAGCGCGAAAAAGTGCCTT 266
                                                                                                                                                                                                                                                                              267 AAAAAGATACGTTTTTACTGGTGACATAGTATTAAAAATAAAAAATTGTCTCAAT 326
                                                                                                                                                                                                                                                                                                                                                                        872 ITCACTCAAACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAGACGGA 931
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.9%; Score 38.2; DB 4; Length 1848;
Best Local Similarity 48.0%; Pred. No. 0.18;
Matches 109; Conservative 0; Mismatches 118; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  932 AGCATGGCTGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAA 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Al, Preeti
APPLICANT: Al, Preeti
APPLICANT: Corley, Neil C.
TILLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPAGE.
OPERATING SYSTEM: DOS
COFTWARE: FASTSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Incyte Pharmaceuticals, Inc.: 3174 Porter Dr.
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0421 US
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/985,335 FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08985335
Patent No. 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                          634 ACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACATCCTTCTCAAATGGC 693
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                                                                                                                       Gaps
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                                                                              Score 37.4; DB 3; Length 2082;
Pred. No. 0.35;
0; Mismatches 111; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                    1607 ATCAGAACAATTTCTACCTTATCCTACTATAGTAA 1573
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                                                                                                                                                                                                                                                                                                                                                                                              814 AACTGGCCGTTTTAAAAGCGGATCTAGAAAAGAAA 848
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                            Ouery Match 1.9%;
Best Local Similarity 48.4%;
Matches 104; Conservative
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2082 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: LATRIUT02
CLONE: 1352286
LATRTUT02
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                  1352286
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  LIBRARY:
    ; LIBRARY:
; CLONE: 1
US-08-985-335-4
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US-09-410-372-4
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Streptococcus pneumoniae Polynucleotides and Sequences 391
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                                                                                                                                                                                                                                                                                       1667 TTAATCAAATGTAAACATATGTTTTCTAACACCAGTATAGAAAATACAAAAACTAATTACA 1608
                                                                                                                                                                                                                      1727 TACTTATAATTAAAGAAAGCTTCCTTTAGCTGGATTACCCTGCATAAATAGGCAACACAG 1668
                                                                                                                            1787 ACAAATGGACAGGCAAGCAGGATAGCATTCTTTGATTACTATAATAGTCACAATAA 1728
                                                                                       634 ACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACATCCTTCTCAAATGGC 693
                                                                                                                                                                          694 AACGICTIACIGAAGAACAGIGCCITITIAGIGCAIGCTITCAGAAAAAGAAGAIGCAG 753
                                                                                                                                                                                                                                                                  754 TGAACAAGATTCACACAACTGGCTTTAAAGATCAAAATGAAATGTTATCAAGTCTTCAAA 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 GCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACATCCTTCTCAAA 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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50.6%; Pred. No. 0.62;
.ive 0; Mismatches 88; Indels C
1.9%; Score 37.4; DB 4; Length 2082;
48.4%; Pred. No. 0.35;
                                           Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP VECTRA 486/33
COMPUTER: HP VECTRA 486/33
                                         0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 212, Application US/08961527
Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
                    Best Local Similarity 48.4%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
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Best Local Similarity 50.6 Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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US-08-961-527-212/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20850
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  Query Match
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- Db 2664 TTGGCTCGTAAAAATGAAGAAATGTACCTCTTACTCTGTAGAAAAAGAAAAC 2605
- ογ
- Search completed: April 25, 2003, 17:45:05 Job time: 91.5741 secs

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Sequence 15766, A Sequence 21956, A Sequence 21083, A Sequence 27715, A Sequence 27715, A Sequence 1877, App Sequence 18355, A Sequence 44, A Sequence 44, A Sequence 44, A Sequence 44, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 442, App
Sequence 442, App
Sequence 4010, Ap
Sequence 92, Appl
                                                                                                            (without alignments)
16376.941 Million cell updates/sec
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Sequence 75,
                                                                                                                                                                                           1 ggcagttcattgatggagag........cattgagccaagtgtccgga 2001
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                                                                                           April 25, 2003, 17:39:49 ; Search time 132.952 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_pUBCOMB.seq:*

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5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-864-761-21956

0 US-09-864-761-1083

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0 US-09-864-761-3277

0 US-09-918-995-24084

0 US-09-918-995-24084

0 US-09-960-253-157

0 US-09-960-253-157

0 US-09-964-761-18355

0 US-09-844-353A-44

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US-10-184-634-442
US-09-960-352-4010
US-09-842-552-92
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                                                                                                                                            US-09-845-416-14_COPY_1000_3000
2001
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 5000
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141.4
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                                                                                                                                                              Title:
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-	Sequence 13, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 13, Appl		Sequence 13, Appl	Sequence 13, Appl			Sequence 264, App	Sequence 4, Appli	Sequence 9459, Ap	Sequence 1, Appli	Sequence 9181, Ap	Seguence 5, Appli	Seguence 126, App	Sequence 420, App	Sequence 2218, Ap	Sequence 345, App	Sequence 282, App	4	Sequence 1145, Ap	'n	Sequence 212, App	Sequence 637, App	
US-09-864-761-8973	US-10-227-884-13	US-10-230-163-13	US-10-218-631-13	US-10-230-338-13	US-10-230-414-13	US-10-216-159A-13	US-10-218-849-13	US-10-227-873-13	US-10-227-883-13	US-09-964-824A-264	US-09-894-657-4	US-09-815-242-9459	US-09-092-218-1	US-09-815-242-9181	US-08-834-666A-5	US-10-043-487-126	US-09-925-301-420	US-09-867-701-2218	US-10-091-483-345	US-10-079-854-282	US-09-764-878-282	US-09-764-860-1145	US-09-764-846-345	US-10-123-155-212	US-10-025-380-637	
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1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	
38.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.2	37.2	37.2	37.2	37	36.8	36.4	36.4	36.4	36.4	36.4	36.4	36	35.6	
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ALIGNMENTS

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE REFERENCE: AGONIGA X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR PILING DATE: 2001-01-30

ESULT 1
US-09-864-761-15766
Squence 15766, Application US/09864761
; Patent No. US20020048763A1
                                                                                                                                                                               PACELL INCORNATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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US-09-861-451A-75 US-09-854-133-728

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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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Best Local Similarity 98.28
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-21956
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LENGTH: 256
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GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Green, Wenshong
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT FILING DATE: 2000-05-204
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,366
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,366
PRIOR APPLICATION NUMBER: DET/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PRIING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15766
LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: MAP TO AC004468.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.41
US-09-864-761-15766
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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US-09-864-761-21956
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Sequence 6092, Application US/09864761

Batent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hancal, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

TITLE OF INVENTION: GDNE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-x-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-05-04

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGCAGTTCATTGATGAGAGAGAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BROWE MARROW, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BOLL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: SYPRESSED IN FILM, SIGNAL = 1.7
OTHER INFORMATION: SYPRESSED IN FILM, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: P11532, EVALUE 2.00e-30
OTHER INFORMATION: WIT HIT: 915032282, EVALUE 1.00e-103
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PRIOR APPLICATION NUMBER: PCT/USO1/00062
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOSTWARE: Annomax Sequence Listing Engine vers: 1.1
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Patent No. US30020048763a1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GTATTATCGTGGCTTCTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAAT 120
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
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Best Local Similarity 100.0%; Pred. No. 2.6e-32;
Matches 144; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2000-09-2/1
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 09/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2000-06-30
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JS-09-864-761-11083
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373 GCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAGGAGCCTCTTGGACCTGATCT 432
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COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.81

US-09-864-761.11083
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CURRENT APPLICATION UNDBER: US/09/864,761
CURRENT APPLICATION UNDBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PAPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR FILING DATE: 2000-06-03
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-10-06-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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RESULT 5

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401 AACAAAAACAGAAGAAGAACAAGGAAAATGGAGGAAGAGCCCTCTTGGACCTGATCTTGA 460
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                     1 TTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAAAGAGTTGAATGACTGGCT 60
                                                                                                                                                                                                                                                               461 AGACCTAAAACGCCAAGTACAACATAAG 491
                                                                                                                                                                                                                                                                                                     121 AGACCTAAAACGCCAAGTACAACAACATAAG 151
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
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N: EXPRESSED IN LUNG, SIGNAL = 0.89
N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.84
N: EXPRESSED IN BRAIN, SIGNAL = 0.96
N: EXPRESSED IN BONE MARROW, SIGNAL = 0.88
N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81
N: WITHIT: MIBS33.1, EVALUE 6.00e-80
N: SWISSPROT HIT: P11532, EVALUE 4.00e-08
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99.3%; Pred. No. 3.7e-31;
tive 0; Mismatches 0; Indels
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LENGTH: 151
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-3
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: F.L.,
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNMBER: PCT/US01/00669
PRIOR ALPILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/234,687
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                              Sequence 27715, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP TO AC004468.1
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                                                                                                                  GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: WOTHER INFORMATION: S'OTHER INFORMATION: S'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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US-09-864-761-27715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-09-864-761-27715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR ```

342 TITACATAGAGITITAATGGAICICCAGAATC-GAAACIGAAAGAGITGAATGACIGGCI 400

```
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 EXPRESSED IN LUNG, SIGNAL = 0.41

EST_HUMAN HIT: BF784138 1., EVALUE 1.60e+00

SWISSPROT HIT: P11532, EVALUE 1.00e-17

NT HIT: X06178.1, EVALUE 9.00e-63
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 32272
LENGTH: 122
 PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PPLING DATE: 2000-10-04
PRIOR PPLING DATE: 2000-10-04
PRIOR PPLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
 FILE REFERENCE: Aeomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCI/US01/00665
 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
 09/774,203
Sequence 32272, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
 OTHER INFORMATION: MAP TO AC004468.1
 2001-01-29
 PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
 APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng
 ORGANISM: Homo sapiens
 OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: S OTHER INFORMATION: N
```

```
-09-864-761-18355
 2247
 TYPE: DNA
 Query Match
 LENGTH:
 òγ
 0;
 1863 TTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGGCAGGCTGGGCCTCCTTCTG 1922
 1803 TITAAAACTGGCATCATITCCCTGTGTAAAGCACATITGGAAGACAAGTACAGATACCTT 1862
 1743 CIGAACIGGCIGCIGAATGITIAIGAIACGGGACGAACAGGGAGGAICCGIGICCIGICI 1802
 258 GTTAAAGCTATGTTAGCAACCATGTGTGGTGGAAAAATGCTGGACAAATTGAGATATGTT 317
 198 CTCAACTTTATGATTGCTGCATATGACAGTGAGGGCCGAGGCAAGTTGACGGTATTTTCA 257
 880 AACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCCAGAAGACGGAAGCATGGC 939
 940 TGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCAC 999
 1923 CATGATTCTATCCAAATTCCAAGACAGTTGGGTGAAGTTGCATCCTTTGGGGGCA 1977
 ;
 2.7%; Score 54.2; DB 9; Length 449;
nilarity 51.9%; Pred. No. 1.3e-05;
Conservative 0; Mismathham
 6.1%; Score 122; DB 10; Length 122; 100.0%; Pred. No. 3.6e-26; Live 0; Mismatches 0; Indels
 Sequence 24084, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: US/09/235,076
 JS-09-960-253-157
Sequence 157, Application US/09960253
Patent No. US20020123619A1
 NAME/KEY: misc_feature
LOCATION: (1)...(449)
OTHER INFORMATION: n = A,T,C or G
 APPLICANT: Benson, Darin R. APPLICANT: Mohamath, Raodoh APPLICANT: Lodes, Michael J.
 Matches 122; Conservative
 ORGANISM: Homo sapiens
 Local Similarity
nes 122; Conserva
 Best Local Similarity
 GENERAL INFORMATION:
 15-09-918-995-24084
S-09-864-761-32272
 18-09-918-995-24084
 1000 AG 1001
 121 AG 122
 TYPE: DNA
 Query Match
 Query Match
 Matches
 ESULT 7
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 g
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
 ö
 1743 CTGAACTGGCTGCTGAATGTTTATGATACGGGACGAACAGGGAGGATCCGTGTCCTGTCT 1802
 1803 TTTAAAACTGGCAFCATTFCCCTGTGTAAAGCACATTTGGAAGACAAGTACAGATACCTT 1862
 1863 TTCAAGCAAGTGGCAAGTTCAACAGGATTTTGTGACCAGGCGAGGCTGGGCCTCCTTCTG 1922
 517 CTCAACTTTATGATTGCTGCATATGACAGTGAGGGCCGAGGCAAGTTGACGGTATTTTCA 576
 637 TICICCCAGAIGICAGATICCAAIGGCTTAAIGATATTTAGCAAGTTTGACCAGTTTCTG 696
 577 GTTAAAGCTATGTTAGCAACCATGTGTGGGAAAAATGCTGGACAAATTGAGATATGTT
 1923 CATGATICTATCCAAATICCAAGACAGTIGGGTGAAGTIGCAICCTITGGGGGCA 1977
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REPERENCE: 210121.556
CURRENT APPLICATION NUMBER: US/09/960,253
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
 Score 54.2; DB 10; Length
Pred. No. 3.8e-05;
0; Mismatches 113; Indels
 CURKENT FILLING DATE: 2001-09-62
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-06-03
PRIOR FILLING DATE: 2000-04-03
PRIOR FILLING DATE: 2000-00-04
PRIOR FILLING DATE: 2000-00-07
PRIOR FILLING DATE: 2000-00-07
PRIOR FILLING DATE: 2000-00-07
PRIOR FILLING DATE: 2000-00-27
PRIOR FILLING DATE: 2001-01-30
 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23
 SOFTWARE: FastSEQ for Windows Version 4.0
 Sequence 18355, Application US/09864761 Patent No. US20020048763A1
 2.7%;
51.9%;
 GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
 Best Local Similarity 51.9
Matches 122; Conservative
 ; ORGANISM: Homo sapiens US-09-960-253-157
```

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237 AGGAAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCA--GATGAATCTCCTAAAT 294
 295 TCAAGATGGGAATGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTT 354
 355 TIAATGGATCTCCAGAATCGAAACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAG 414
 415 AAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTGAAGACCTGAAAACGCC 474
 2; Gaps
 Query Match 2.3%; Score 45.2; DB 10; Length 423; Best Local Similarity 49.7%; Pred. No. 0.0057; Matches 143; Conservative 0; Mismatches 143; Indels 2
 N: EXPRESSED IN HBL100, SIGNAL = 3.1
N: EXPRESSED IN HBLLA, SIGNAL = 2.8
N: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
N: EXPRESSED IN LUNG, SIGNAL = 1.4
N: EXPRESSED IN FEATH LIVER, SIGNAL = 2.6
N: EXPRESSED IN HEART, SIGNAL = 3.2
N: EXPRESSED IN PRACENTA, SIGNAL = 3.2
N: EXPRESSED IN PLACENTA, SIGNAL = 1.9
N: EXPRESSED IN PLACENTA, SIGNAL = 1.9
N: EXPRESSED IN BADIT LIVER, SIGNAL = 1.9
N: EXPRESSED IN BT474, SIGNAL = 2.6
 475 AAGTACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAG 522
 APPLICANT: Buykun, Gary
APPLICANT: Ogg, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
 NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18355
 FILE REFERENCE: 00766/351004
CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT APPLICATION NUMBER: US/09/205,658
EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1997-07-07
 MAP TO AC010133.1
EXPRESSED IN HBL100,
 APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
 APPLICATION NUMBER: PCT/US01/00670
 PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNMBER: US 60/234,687
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
 PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
 IS-09-205-658-44/C
Sequence 44, Application US/09205658
Patent No. US20010029617A1
GENERAL INFORMATION:
FILING DATE: 2001-01-30
 ORGANISM: Homo sapiens
 OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-864-761-18355
 OTHER INFORMATION: OTHER INFORMATION:
 INFORMATION:
INFORMATION:
 OTHER INFORMATION:
OTHER INFORMATION:
 INFORMATION:
 TYPE: DNA
 OTHER
OTHER
 RESULT 10
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 0;
 2056 CAAGAAATCAAATTTTTTGAAAAATTCAATTAAAAAGACAGATTGGGGAATGTGTTTTA 1997
 2116 GCTAGACATTTGCTACCAGGGGAAAAAAAAGAGGAAAATTAAAGAATTACAAGAGAAAT 2057
 1996 GCAGTTTTGATTGCAAACAAATTTACAGCGAAAAAGATGGGATAGAGGTAGCATTTAAA 1937
 376 AACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGG 435
 2116 GCTAGACATTIGCTACCAGGGGAAAAAAAAGAGGAAAATTAAAAGAATTACAAGAGAAAT 2057
 2056 CAAGAAATCAAATTTTTGAAAAATTCAATTAAAAAGACAGATTGGGGAATGTTTTA 1997
 196 GITGGTAATATICTACAATIGGGAAGTAAGCTGATIGGAACAGGAAAATTATCAGAAGAT 255
 256 GAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGG 315
 316 GTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCGA 375
 196 GITGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGAT 255
 256 GAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGG 315
 0; Gaps
 2.1%; Score 42.4; DB 10; Length 2704; 48.4%; Pred. No. 0.14;
 2.1%; Score 42.4; DB 10; Length 2704;
48.4%; Pred. No. 0.14;
tive 0; Mismatches 126; Indels 0;
 0; Mismatches 126; Indels
 APPLICANT: Koweek, Allison
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351005
 CURRENT APPLICATION NUMBER: US/09/844,353A CURRENT FILING DAFE: 2001-04-27
PRIOR APPLICATION NUMBER: US 08/857,076
PRIOR FILING DATE: 1997-05-15
EARLIER FILLING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSEQ for Windows Version 4.0
 NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSEQ for Windows Version 4.0
 Sequence 44, Application US/09844353A Patent No. US20020037585A1
 ; ORGANISM: Caenorhabditis elegans US-09-205-658-44
 TYPE: DNA ORGANISM: Caenorhabditis elegans
 APPLICANT: Patterson, Garth
APPLICANT: 099, Scott
PAPLICANT: Paradis, Susanne
APPLICANT: Tissenbaum, Heidi
 Kimura, Koutarou
 Matches 118; Conservative
 Query Match
Best Local Similarity 48.4%
Matches 118; Conservative
 APPLICANT: Morris, Jason
 GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
 Best Local Similarity
 1876 AATA 1873
 US-09-844-353A-44/C
 436 AAGA 439
 US-09-844-353A-44
 2704
 SEQ ID NO 44
TRNGTH: 2704
 SEQ ID NO 44
 TYPE: DNA
 Query Match
 APPLICANT:
 LENGTH:
 qq
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 Dp
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Ogg, Scott
 GENERAL INFORMATION:
 2671 AATA 2668
 US-10-184-644-442/c
 436 AAGA 439
 US-09-844-353A-43
 SEQ ID NO 43
LENGTH: 3499
 APPLICANT:
 APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT: APPLICANT:
 APPLICANT:
 APPLICANT:
 TYPE: DNA
 APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT:
 RESULT 14
 qq
 δλ
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 2851 CAAGAAATCAAATTTTTGAAAATTCAATTAAAAAGACAGATTGGGGAATGTGTTTA 2792
 2791 GCAGTTTTGATTGCGAAACAAATTTACAGCGAAAAAGATGGGATAGAGGTAGCATTTAAA 2732
 2911 GCTAGACATTIGCTACCAGGGGGAAAAAAAAAGGGGAAAATTAAAAGAATTACAAGAAAT 2852
 316 GTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCGA 375
 376 AACTGAAAGAGTTGAATGACTGGCTAACAAAAACAGAAGAAGAACAAGGAAAATGGAGG 435
 256 GAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGG 315
 196 GTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGAT 255
 1996 GCAGTITTGATTGCGAAACAAATTTACAGCGAAAAGATGGGATAGAGGTAGCATTTAAA 1937
 Gaps
 316 GIAGCTAGCATGGAAAAAAAAAGCAATTTAACATAGAGTTTTAATGGATCTCCAGAATCGA 375
 .
0
 Query Match 2.1%; Score 42.4; DB 10; Length 3499; Best Local Similarity 48.4%; Pred. No. 0.17; Matches 118; Conservative 0; Mismatches 126; Indels 0;
 APPLICANT: Ogg, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
 CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER FILING DATE: 1997-07-07
EARLIER PLICATION NUMBER: 08/888,534
EARLIER APPLICATION NUMBER: US/98/10080
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FASCEQ for Windows Version 4.0
SEQ ID NO 43
 Sequence 43, Application US/09205658 Patent No. US20010029617A1
 ORGANISM: Caenorhabditis elegans
JS-09-205-658-43
 GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
 2671 AATA 2668
 1876 AATA 1873
 436 AAGA 439
 436 AAGA 439
 ESULT 12
S-09-205-658-43/c
 3499
 LENGTH:
```

```
2851 CAAGAAATCAAATTTTTGAAAATTCAATTAAAAAGACAGATTGGGGAATGTGTTTA 2792
 2911 GCTAGACATTTGCTACCAGGGGAAAAAAAAGAGGAAAATTAAAAGATTACAAGAAAT 2852
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
 256 GAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAATGCCTCAGG 315
 316 GTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCGA 375
 196 GTTGGTAATATTCTACAATTGGGAAGTAAGCTGATTGGAACAGGAAAATTATCAGAAGAT 255
 Query Match Best Local Similarity 48.4%; Pred. No. 0.17; Matches 118; Conservative 0; Mismatches 126; Indels 0;
 APPLICANT: Koweek, Allison
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351005
CURRENT APPLICATION NUMBER: US/09/844,353A
CURRENT FILING DATE: 2001-04-27
PRIOR PILICATION NUMBER: US 08/857,076
PRIOR FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FASTSEQ for Windows Version 4.0
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
 CURRENT APPLICATION NUMBER: US/10/184,644 CURRENT FILING DATE: 2002-06-28
 Sequence 442, Application US/10184644 Publication No. US20030044930A1
 ORGANISM: Caenorhabditis elegans
 Pan, James
Smith, Victoria
Watanabe, Colin K.
 Godowski, Paul J.
Gurney, Austin L.
Paradis, Suzanne
Tissenbaum, Heidi
 Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Morris, Jason
 Zhang, Zemin
 ORGANISM: Homo Sapien
 SEQ ID NO 442
 TYPE: PRT
```

US-10-184-644-442

Sequence 43, Application US/09844353A Patent No. US20020037585A1

US-09-844-353A-43/C

RESULT 13

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APPLICANT: Ruvkun, Gary APPLICANT: Kimura, Koutarou APPLICANT: Patterson, Garth

GENERAL INFORMATION:

0

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0
 1263 GACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTG 1322
 1383 GGTCCCTGGGAGAGGCCATCTCGCCAAACAAAGTGCCCTACTATATCAACCACGAGACT 1442
 1443 CAAACAACTTGCTGGGACCATCCCAAAATGACAGAGCTCTACCAGTCTTTAGCTGACCTG 1502
 1503 AATAATGTCAGATTCTCAGCTTATAGGACTGCCATGAAACTCCGAAGACTGCAGAAGGCC 1562
 1563 CTTTGCTTGGATCTCTTGAGCCTGTGAGCTGCATGTGATGCCTTGGACCAGCACAACCTC 1622
 369 T...CYKHK..NHRCDWCY.WC.YYCASNKW...K.YN.A..WC.HTB.A..SB.MCMMR 310
 309 R.YS..T.M.RBAKD.BAS.MNR..SDMC.T.W.SBB.CYHMB...HN.S.RMN...BMH 250
 0; Gaps
 249 KW..HAKCDHS...BN.YH..CY...WMAKRW.BAHBTW.THMY..ST.CRDDC.BH.Y. 190
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
 1263 GACCTGAACACCAGATGGAAGCTTCTGCAGGTGGCCGTCGAGGACCGAGTCAGGCAGCTG 1322
 129 MA.ABW...SCNWW..K.SHMNBC.H.SMNAA.HWKRNC.K.DB.GDYCAK.ARRN.RS. 70
 |:::: || ::| |::| |::| |::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |::
Query Match 2.1%; Score 41.8; DB 9; Length 440; Best Local Similarity 8.7%; Pred. No. 0.06; Matches 33; Conservative 132; Mismatches 214; Indels
 ch 2.1%; Score 41.8; DB 9; Length 440; 1 Similarity 8.7%; Pred. No. 0.06; 33; Conservative 132; Mismatches 214; Indels (
 CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
 Sequence 442, Application US/10184634
Publication No. US20030068684Al
GENERAL INFORMATION:
 1623 AAGCAAAATGACCAGCCCA 1641
 : | ::::| :: :
69 S..H.A.RHBMBCYSB..M 51
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
 Desnoyers, Luc
 ORGANISM: Homo Sapien
 Chen,Jian
 Pan, James
 Best Local Similarity
 JS-10-184-634-442/C
 -10-184-634-442
 APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 TYPE: PRT
 Query Match
 APPLICANT:
 APPLICANT:
 APPLICANT
 Matches
 g
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Db 369 T...CYKHK..NHRCDWCY.WC.YYCASNKW...K.YN.A..WC.HTB.A..SB.MCMMR 310

Qy 1383 GGTCCCTGGGAGAGACACTCTCGCCAAACAAAGTGCCCTACTATACAACCACGAGACT 1442

Db 309 R.YS..T.M.RBAKD.BAS.MNR..SDMC.T.W.SBB.CYHMB...HN.S.RMN...BMH 250

QY 1443 CAAACAACTTGCTGGGACATCCCAAAATGACAGAGTCTTAAGCTGACTG 1502

Db 249 KW..HAKCDHS...BN.YH..CY...WMAKRW.BAHBTW.THMY..ST.CRDDC.BH.Y. 190

QY 1503 AATAATGTCAGATTCTCAGCTTATAGGACTGCCAAAAGGCC 1562

Db 189 DR.TT.HTYCSM.SH.THSBTNT.N.HA.BNMR..GRA.YBC...B.GC.WRKRBBWYMT 130

QY 1563 CTTTGCTTGAGTCTTTAGGCTGCATGAATGCTTGGACGACAACCTC 1622

Db 129 MA.ABW...SCNWW.K.SHMNBC.H.SMNAA.HWKRNC.K.DB.GDYCAK.ARRN.RS. 70

QY 1623 AAGCAAAATGACCACCACAACTGATGCATGCATGCAACACCTC 1622

Db 69 S..H.A.RHBMBCYSB..M 51

Search completed: April 25, 2003, 23:58:46
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